

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 2, 2006, 03:53:56 ; Search time 48 Seconds
(without alignments)
1216.021 Million cell updates/sec

Title: US-10-755-889-18

Perfect score: 3793 1 MASPADSCIOFTRHSDVLL.....TKVQYRVSATDLPPELPKAC 706

Sequence: 1 MASPADSCIOFTRHSDVLL.....TKVQYRVSATDLPPELPKAC 706

Scoring table: BLOSUM62

Searched: Gapop 10.0, Gapext 0.5

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patente AA.*
1: /cgn2_6/ptodata/1/1aa/5_COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/6_COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/H_COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/PTUS_COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	3777	99.6	706 2	US-09-538-092-1104
2	3763	99.2	706 1	US-08-074-967-2
3	3763	99.2	706 1	US-08-553-541B-2
4	3763	99.2	706 2	US-09-268-202-2
5	3763	99.2	706 2	US-09-761-117-2
6	3763	99.2	706 4	PCT-US94-06669-2
7	602	15.9	803 2	US-09-063-035-2
8	560	14.8	110 1	US-08-553-541B-9
9	560	14.8	110 1	US-09-268-202-9
10	540	14.2	733 2	US-09-761-117-9
11	540	14.2	733 2	US-09-949-016-7651
12	538	14.2	106 1	US-08-340-203A-10
13	538	14.2	106 1	US-08-452-427-10
14	538	14.2	106 1	US-09-085-407-10
15	508	13.4	678 2	US-09-949-016-10273
16	503	13.3	799 2	US-10-104-047-29229
17	501	13.2	673 2	US-09-538-092-1270
18	483	12.7	488 1	US-08-933-750C-17
19	483	12.7	488 2	US-09-234-613-17
20	481	12.7	685 2	US-09-949-016-8627
21	478.5	12.6	1191 2	US-09-949-016-6356
22	477	12.6	656 2	US-09-949-016-10075
23	477	12.6	769 2	US-09-949-016-8149
24	476	12.5	458 2	US-09-538-092-1356
25	469	12.4	541 2	US-10-104-047-2161
26	468.5	12.4	540 2	US-10-104-047-3748
27	468	12.3	803 2	US-09-538-092-1026

28	465.5	12.3	781 2	US-10-104-047-2937	Sequence 2937, Ap
29	465	12.3	586 2	US-10-104-047-2592	Sequence 2592, Ap
30	465	12.3	698 2	US-09-949-016-11419	Sequence 11419, A
31	464.5	12.2	746 2	US-09-949-016-11494	Sequence 11494, A
32	463	12.2	556 2	US-10-104-047-3914	Sequence 3914, Ap
33	458.5	12.1	561 2	US-10-104-047-3434	Sequence 2805, Ap
34	458	12.1	530 2	US-10-104-047-3434	Sequence 3434, Ap
35	457	12.0	409 2	US-10-104-047-2663	Sequence 2663, Ap
36	457	12.0	475 2	US-10-104-047-3470	Sequence 3470, Ap
37	455	12.0	429 2	US-10-104-047-2786	Sequence 2786, Ap
38	454.5	12.0	469 2	US-09-538-092-1195	Sequence 1195, Ap
39	454.5	12.0	504 2	US-10-104-047-2053	Sequence 2053, Ap
40	454	12.0	636 2	US-10-104-047-2449	Sequence 2449, Ap
41	451.5	11.9	639 2	US-09-949-016-9434	Sequence 9434, Ap
42	445	11.7	643 2	US-10-104-047-2241	Sequence 2241, Ap
43	444.5	11.7	638 2	US-09-949-016-11391	Sequence 11391, A
44	442.5	11.7	592 2	US-10-104-047-3366	Sequence 3366, Ap
45	442	11.7	292 2	US-09-538-092-1334	Sequence 1334, Ap

ALIGNMENTS

RESULT 1
US-09-538-092-1104
Sequence 1104, Application US/09538092
Patent No. 675314
GENERAL INFORMATION:
APPLICANT: Glot, Iolc
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuratSeqFormatter Version 0.9
SEQ ID NO 1104
LENGTH: 706
TYPE: PRT
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: misc.feature
LOCATION: (0)..(0)
OTHER INFORMATION: Polypeptide Accession Number P41182
US-09-538-092-1104
Query Match 99.6%; Score 3777; DB 2; Length 706;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 703; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
1 MASPADSCIOFTRHSDVLLNLRSDITLVIVVSRQFAHTVLMACGLFYSI 60
1 MASPADSCIOFTRHSDVLLNLRSDITLVIVVSRQFAHTVLMACGLFYSI 60
1 MASPADSCIOFTRHSDVLLNLRSDITLVIVVSRQFAHTVLMACGLFYSI 60
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FTDQKNSLVINIDPEINPEGFCILDFMTYSLNREGINAVMATYMLQNEHVDI 120
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CRRTKASAEVMSAIKPRREFINSMLMPQDIIMAYRGREVENNTPLNSAPCESRAF 180
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APSYISGLSTPPASVMSHLPVSSLLFSDSEFPDVPANPPKERRALPCDSARPYPG 240
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EYSPTLEVSFNVCHSNISYSPKETIPEEASDMHYVAEGIKPAAPSAAPNPPPCDKAS 300

QY 301 KEEBSSSEDEIALHFEPPNAPLNKGLVSPQSPKSDCOPNSPTACSSKNACILQASG 360
DB 301 KEEBSSSEDEIALHFEPPNAPLNKGLVSPQSPKSDCOPNSPTACSSKNACILQASG 360
QY 361 SPAPSPDPKACNMKKYKFIYVNSLONAKPGPBOAELGRLSPRAYTAPACOPMPER 420
DB 361 SPAPSPDPKACNMKKYKFIYVNSLONAKPGPBOAELGRLSPRAYTAPACOPMPER 420
QY 421 ENLDIOSPTKLSASGEDSTIPQASRLNNTVNRSMTPSPSSSSSHPLVMPKCTSCS 480
DB 421 ENLDIOSPTKLSASGEDSTIPQASRLNNTVNRSMTPSPSSSSSHPLVMPKCTSCS 480
QY 481 QSPHAEMLCHTAGPTFAEMGETOSEYSDSCENGAFPCNECDCFSEBASLKHRTLOT 540
DB 481 QSPHAEMLCHTAGPTFAEMGETOSEYSDSCENGAFPCNECDCFSEBASLKHRTLOT 540
QY 541 HSDKPYKCDRCQASFRYKGNLASHKTVHTGEKPYPCNICGAQPNRPANLKTHTRIHSGEK 600
DB 541 HSDKPYKCDRCQASFRYKGNLASHKTVHTGEKPYPCNICGAQPNRPANLKTHTRIHSGEK 600
QY 601 PYKCTCGARFVQVAHLRAHVLHTGEKPYPCNICGTRFRHLQTLKSHLRHTGEKPYPC 660
DB 601 PYKCTCGARFVQVAHLRAHVLHTGEKPYPCNICGTRFRHLQTLKSHLRHTGEKPYPC 660
QY 661 EKCNLFRRKSQLRLRLRQKGAITNTKVQYVSATDLPPELPKAC 706
DB 661 EKCNLFRRKSQLRLRLRQKGAITNTKVQYVSATDLPPELPKAC 706

RESULT 2

US-08-074-967-2
Sequence 2, Application US/08074967
Patent No. 5641672

GENERAL INFORMATION:

APPLICANT: Dalia-Favera, Riccardo

APPLICANT: Chaganti, R.S.K.

TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS

TITLE OF INVENTION: bcl-6

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESS: Cooper & Dunham

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: New York

COUNTRY: United States of America

ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/074,967

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 0575/43771

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 977-9550

TELEFAX: (212) 664-0525

TELEX: 422523 COOP UI

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 706 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-074-967-2
Query Match 99.2%; Score 3763; DB 1; Length 706;

Best Local Similarity 99.3%; Pred. No. 0;
Matches 701; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MASPDSCIQFTRHARDVILNLRSRDILTDVYIVSRBQFRHAKTYLMAQGLFYSI 60
DB 1 MASPDSCIQFTRHARDVILNLRSRDILTDVYIVSRBQFRHAKTYLMAQGLFYSI 60
QY 61 FTDOAKCNLSVINLDEINPEGCILDPMTYSTRNLREGINMAYMATMYLQMEHYVD 120
DB 61 FTDOAKCNLSVINLDEINPEGCILDPMTYSTRNLREGINMAYMATMYLQMEHYVD 120
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DB 121 CKKFKASBAEYVSAIKPPREFLNSRMLMPDIDIAAYGRVENVNLPRLSAPGESAPF 180
QY 181 ABSLYSGISTPASTSMYSHLTVSSILFSDSEFRDVRVNPANPFEKERALPCDSARPYG 240
DB 181 ABSLYSGISTPASTSMYSHLTVSSILFSDSEFRDVRVNPANPFEKERALPCDSARPYG 240
QY 241 EYSRPTLEVPVCHSNITSPKETIPPEARSDMHSVAEGLKPAAPSRANAPYPCDYAS 300
DB 241 EYSRPTLEVPVCHSNITSPKETIPPEARSDMHSVAEGLKPAAPSRANAPYPCDYAS 300
QY 301 KEEBSSSEDEIALHFEPPNAPLNKGLVSPQSPKSDCOPNSPTACSSKNACILQASG 360
DB 301 KEEBSSSEDEIALHFEPPNAPLNKGLVSPQSPKSDCOPNSPTACSSKNACILQASG 360
QY 361 SPAPSPDPKACNMKKYKFIYVNSLONAKPGPBOAELGRLSPRAYTAPACOPMPER 420
DB 361 SPAPSPDPKACNMKKYKFIYVNSLONAKPGPBOAELGRLSPRAYTAPACOPMPER 420
QY 421 ENLDIOSPTKLSASGEDSTIPQASRLNNTVNRSMTPSPSSSSSHPLVMPKCTSCS 480
DB 421 ENLDIOSPTKLSASGEDSTIPQASRLNNTVNRSMTPSPSSSSSHPLVMPKCTSCS 480
QY 481 QSPHAEMLCHTAGPTFAEMGETOSEYSDSCENGAFPCNECDCFSEBASLKHRTLOT 540
DB 481 QSPHAEMLCHTAGPTFAEMGETOSEYSDSCENGAFPCNECDCFSEBASLKHRTLOT 540
QY 541 HSDKPYKCDRCQASFRYKGNLASHKTVHTGEKPYPCNICGAQPNRPANLKTHTRIHSGEK 600
DB 541 HSDKPYKCDRCQASFRYKGNLASHKTVHTGEKPYPCNICGAQPNRPANLKTHTRIHSGEK 600
QY 601 PYKCTCGARFVQVAHLRAHVLHTGEKPYPCNICGTRFRHLQTLKSHLRHTGEKPYPC 660
DB 601 PYKCTCGARFVQVAHLRAHVLHTGEKPYPCNICGTRFRHLQTLKSHLRHTGEKPYPC 660
QY 661 EKCNLFRRKSQLRLRLRQKGAITNTKVQYVSATDLPPELPKAC 706
DB 661 EKCNLFRRKSQLRLRLRQKGAITNTKVQYVSATDLPPELPKAC 706

RESULT 3

US-08-553-541B-2
Sequence 2, Application US/08553541B
Patent No. 5882858

GENERAL INFORMATION:

APPLICANT: Dalia-Favera, Riccardo

APPLICANT: Chaganti, Raju S.K.

TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS

TITLE OF INVENTION: bcl-6

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESS: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: United States of America

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/553,541B
 FILING DATE: May 28, 1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 0575/43771-A-PCT-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 278-0400
 TELEFAX: (212) 391-0525
 TELEX: 422523 COOP UI
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 706 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-553-541B-2

Query Match 99.3%; Score 3763; DB 1; Length 706;
 Best Local Similarity 99.3%; Pred. No. 0;
 Matches 701; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

1 MASPADSCIOFTRHARDVLTNLRSDILTDVIVVSRQFRAKTVLMACSGLFYSI 60
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 421 ENLDQSPFKLSASGEDSTIPOASRLNINVRSMTGSRSSSESGSPLYMPPKTS 480
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 481 OSPQHAEMCITAGTFAEMGEQOSESDSSCENGAFFCNCDFESEAISKHTLOT 540
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 601 PYKCTCGARFQVVAHLRAHVLITGEXRYPCEIGTRFRHLQTLKSHLRINTGK 660
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 661 EKCNIHFRHKSQRLRLHROKHGALINTVQVYVSATDLPRLPKAC 706
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 661 EKCNIHFRHKSQRLRLHROKHGALINTVQVYVSATDLPRLPKAC 706

RESULT 4

US-09-268-202-2

Sequence 2, Application US/09268202

Patent No. 6174997

GENERAL INFORMATION:

APPLICANT: Dalia-Favera, Riccardo

TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESS: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: United States of America

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/268,202

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 0575/43771-A-PCT-US-2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 278-0400

TELEFAX: (212) 391-0525

TELEX: 422523 COOP UI

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 706 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-268-202-2

Query Match 99.2%; Score 3763; DB 2; Length 706;

Best Local Similarity 99.3%; Pred. No. 0;

Matches 701; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

1 MASPADSCIOFTRHARDVLTNLRSDILTDVIVVSRQFRAKTVLMACSGLFYSI 60
 1 MASPADSCIOFTRHARDVLTNLRSDILTDVIVVSRQFRAKTVLMAMRGLEFSI 60
 61 FTDLKCNLSVINLDPINDEGFCILLDFMTSLNLRGINAMVATMYLQEHVDT 120
 61 FTDLKCNLSVINLDPINDEGFCILLDFMTSLNLRGINAMVATMYLQEHVDT 120
 121 CRKTIKASEAMWSAIPREEFNSRLMPDIMAARGREVENNPLRSAPCESRAF 180
 121 CRKTIKASEAMWSAIPREEFNSRLMPDIMAARGREVENNPLRSAPCESRAF 180
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 181 APSLYSGISTPPASYSWYSHLPVSSLLFSDDEFDVMPPANPPKRALPCDSARVP 240
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 241 EYSRPTLEVPNVCHSNISYSPKETIPEEASDMHYVAEGIKPAAPARNAFYPCDKAS 300
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 301 KEERPSSEDEIHALHFEPPNAPLNKGLVSPQSPQKDCOPNSTEACSSKNAACILQSG 360
 301 KEERPSSEDEIHALHFEPPNAPLNKGLVSPQSPQKDCOPNSTEACSSKNAACILQSG 360
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 361 SPPAKSPDPPKACWKKYKFTVLSLNOMAKPGGEQALGRLSPRAYTAPACOPMP 420
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Db 361 SPPAKSPTDPRKACSMKKYKFIVLNSLNQNAKPGGPEQAEGLSPRAYTAPACOPMPER 420
Qy 421 ENLDLQSPFKLSASGSDSTIPQASRLNNIVNSMTGSPSSSSSHSPLYMHPPKCTSCGS 480
Db 421 ENLDLQSPFKLSASGSDSTIPQASRLNNIVNSMTGSPSSSSSHSPLYMHPPKCTSCGS 480
Qy 481 OSPOHAEMLHTAGTFAEBMGETOSEYSDSCENGAFPCNECDGCFSEBASLKHHTLTOT 540
Db 481 OSPOHAEMLHTAGTFAEBMGETOSEYSDSCENGAFPCNECDGCFSEBASLKHHTLTOT 540
Qy 541 HSDKPYKCDRCQASFRYKGNLASHKTVHTGKPYRCNICGAQPNRPAULKTHTRHSGEK 600
Db 541 HSDKPYKCDRCQASFRYKGNLASHKTVHTGKPYRCNICGAQPNRPAULKTHTRHSGEK 600
Qy 601 PYCETCGARFQVAVHLRAHVLHTGKPYPCICGTFRRLQTLKSHIRHTGKPYHC 660
Db 601 PYCETCGARFQVAVHLRAHVLHTGKPYPCICGTFRRLQTLKSHIRHTGKPYHC 660
Qy 661 EKCNLFHRKSQLRLHROKGAITNTKVQYRVSATDLPPELPKAC 706
Db 661 EKCNLFHRKSQLRLHROKGAITNTKVQYRVSATDLPPELPKAC 706

RESULT 5

US-09-761-117-2
Sequence 2, Application US/09761117
Patent No. 6783945
GENERAL INFORMATION:
APPLICANT: Dalia-Favera, Riccardo
Chaganti, Raju S.K.
TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS
bcl-6
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/761,117
FILING DATE: 16-Jan-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/43771-A-PCT-US-Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 706 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-761-117-2

Query Match 99.2%; Score 3763; DB 2; Length 706;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 701; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy 1 MASPADSCIOFTIRASDVLTNLNRLRSRDLITDVVIVSREOPRAKTVLMACSGLYSI 60
Db 1 MASPADSCIOFTIRASDVLTNLNRLRSRDLITDVVIVSREOPRAKTVLMACSGLYSI 60

Qy 61 FTDLKCNLSVTLNLDPEINPBGFCILDFMTYSRLNLRBGNIMAYMATAMYLQMEHVDT 120
Db 61 FTDLKCNLSVTLNLDPEINPBGFCILDFMTYSRLNLRBGNIMAYMATAMYLQMEHVDT 120
Qy 121 CRKFKASEAEWVSAIKPREBEFLNSRLMPODINAYGREVENNPLRSAPGESRAF 180
Db 121 CRKFKASEAEWVSAIKPREBEFLNSRLMPODINAYGREVENNPLRSAPGESRAF 180
Qy 181 APSLYGSLSTPPASYSMTSHLPVSSLPSDEEFVRNRPVNPFPKRALPCDSARPVG 240
Db 181 APSLYGSLSTPPASYSMTSHLPVSSLPSDEEFVRNRPVNPFPKRALPCDSARPVG 240
Qy 241 EYSRPTLAVSPVHCNSNIYSPKETIPEARSDDHVSVAEGLKPAASRNAPYPCDQAS 300
Db 241 EYSRPTLAVSPVHCNSNIYSPKETIPEARSDDHVSVAEGLKPAASRNAPYPCDQAS 300
Qy 301 KEERPPSSDEIALHFEPPNAPLNKGLVSPQSPKSDCQPSPTBACSSKNACILQASG 360
Db 301 KEERPPSSDEIALHFEPPNAPLNKGLVSPQSPKSDCQPSPTBACSSKNACILQASG 360
Qy 361 SPPAKSPTDPRKACSMKKYKFIVLNSLNQNAKPGGPEQAEGLSPRAYTAPACOPMPER 420
Db 361 SPPAKSPTDPRKACSMKKYKFIVLNSLNQNAKPGGPEQAEGLSPRAYTAPACOPMPER 420
Qy 421 ENLDLQSPFKLSASGSDSTIPQASRLNNIVNSMTGSPSSSSSHSPLYMHPPKCTSCGS 480
Db 421 ENLDLQSPFKLSASGSDSTIPQASRLNNIVNSMTGSPSSSSSHSPLYMHPPKCTSCGS 480
Qy 481 OSPOHAEMLHTAGTFAEBMGETOSEYSDSCENGAFPCNECDGCFSEBASLKHHTLTOT 540
Db 481 OSPOHAEMLHTAGTFAEBMGETOSEYSDSCENGAFPCNECDGCFSEBASLKHHTLTOT 540
Qy 541 HSDKPYKCDRCQASFRYKGNLASHKTVHTGKPYRCNICGAQPNRPAULKTHTRHSGEK 600
Db 541 HSDKPYKCDRCQASFRYKGNLASHKTVHTGKPYRCNICGAQPNRPAULKTHTRHSGEK 600
Qy 601 PYCETCGARFQVAVHLRAHVLHTGKPYPCICGTFRRLQTLKSHIRHTGKPYHC 660
Db 601 PYCETCGARFQVAVHLRAHVLHTGKPYPCICGTFRRLQTLKSHIRHTGKPYHC 660
Qy 661 EKCNLFHRKSQLRLHROKGAITNTKVQYRVSATDLPPELPKAC 706
Db 661 EKCNLFHRKSQLRLHROKGAITNTKVQYRVSATDLPPELPKAC 706

RESULT 6

PCT-US94-06669-2
Sequence 2, Application PC/TUS9406669
GENERAL INFORMATION:
APPLICANT: Dalia-Favera, Riccardo
Chaganti, R.S.K.
TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS
bcl-6
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06669
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/074,967

FILING DATE: 09-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 43771-A-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 706 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-06669-2

Query Match 99.2%; Score 3763; DB 4; Length 706;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 701; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MASPAUSCIPTFRASDVNLNLRSGRDLITDVIVSREOPRAKTVLMACSGLFYSI 60
DB 1 MASPAUSCIPTFRASDVNLNLRSGRDLITDVIVSREOPRAKTVLMACSGLFYSI 60
QY 61 FTDLKCNLSVINLNDPEINPEGFCILDFMTYSRLNREGNIMAVMATYLMQEHVDT 120
DB 61 FTDLKCNLSVINLNDPEINPEGFCILDFMTYSRLNREGNIMAVMATYLMQEHVDT 120
QY 121 CRKFKASAEAMWSAIPREPEFLNSRMLMPODIMAYRGREVENNIPLSAPGCEERAP 180
DB 121 CRKFKASAEAMWSAIPREPEFLNSRMLMPODIMAYRGREVENNIPLSAPGCEERAP 180
QY 181 APSLYSGISTPPASYSVSHLPVSSLLFSDSEFSDVMPVAPNPPKERRALPCDSARPVG 240
DB 181 APSLYSGISTPPASYSVSHLPVSSLLFSDSEFSDVMPVAPNPPKERRALPCDSARPVG 240
QY 241 EYSRPTLEVPNVCHSNISPKETIPREASDMHYSAEGLKPAAPARNAAPYPCDKAS 300
DB 241 EYSRPTLEVPNVCHSNISPKETIPREASDMHYSAEGLKPAAPARNAAPYPCDKAS 300
QY 301 KEERPSSEDEIALHFEPPNAPLNKGLVSPQSPQSDCOPNSTEACSSKNACILQASG 360
DB 301 KEERPSSEDEIALHFEPPNAPLNKGLVSPQSPQSDCOPNSTEACSSKNACILQASG 360
QY 361 SPPAKSPTDPPKACMKKKYKFTVLSNLQNAKPGGPEQAEIGRLSPRAYTAPACOPMPER 420
DB 361 SPPAKSPTDPPKACMKKKYKFTVLSNLQNAKPGGPEQAEIGRLSPRAYTAPACOPMPER 420
QY 421 ENLLOSPTKLSASGSDSTIPQASRLNNIVNRSMTGSPRSSSESHSPLYMHPKCTSGS 480
DB 421 ENLLOSPTKLSASGSDSTIPQASRLNNIVNRSMTGSPRSSSESHSPLYMHPKCTSGS 480
QY 481 QSPHAEWCLHTAGPTFAEWEGETOSEYSDSSCENGAFFCNECDRCRSEASLKRHTLOT 540
DB 481 QSPHAEWCLHTAGPTFAEWEGETOSEYSDSSCENGAFFCNECDRCRSEASLKRHTLOT 540
QY 541 HSDPYKCDRCOASFRYKGNLASHKTVTGKPYRCNCGAOFNRPALTKHTTHISEK 600
DB 541 HSDPYKCDRCOASFRYKGNLASHKTVTGKPYRCNCGAOFNRPALTKHTTHISEK 600
QY 601 PYKETGARGFYVAHJBAHYLHTGKPYRCEICGTRFRHLOTLSHLRHTGKPYHC 660
DB 601 PYKETGARGFYVAHJBAHYLHTGKPYRCEICGTRFRHLOTLSHLRHTGKPYHC 660
QY 661 ECKNLHFRHKSQRLHLRQKHGAITNTVQYRVSAITDLPPELPKAC 706
DB 661 ECKNLHFRHKSQRLHLRQKHGAITNTVQYRVSAITDLPPELPKAC 706

RESULT 7
US-09-063-035-2
Sequence 2, Application US/09063035

Patent No. 616091
GENERAL INFORMATION:
APPLICANT: PECKERT, Karen; HAENEL, Frank; and EILERS,
APPLICANT: Martin
TITLE OF INVENTION: Myc-binding zinc finger proteins,
TITLE OF INVENTION: their preparation and their use
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: Kell & Weinlauf
STREET: 1101 Connecticut Avenue
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.2 Mb storage
COMPUTER: IBM AT-compatible, 80486 processor
OPERATING SYSTEM: MS-DOS version 6.1
SOFTWARE: Wordperfect version 8.0
CURRENT APPLICATION DATA:
FILING DATE: 21-Apr-1998
CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 803 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-063-035-2

Query Match 15.9%; Score 602; DB 2; Length 803;
Best Local Similarity 26.2%; Pred. No. 2,2e+45; Indels 156; Gaps 23;
Matches 196; Conservative 100; Mismatches 297;

QY 9 IOFTRASDVNLNLRSGRDLITDVIVSREOPRAKTVLMACSGLFYSITDOLKCN 68
DB 1 MDPPQSHVLEBQNOQROGLDCTFVVDGVHFAKRAVLAACTEYFQGLFVDQ 56
QY 69 LSVINLDEINPEGFCILDFMTYSRLNREGNIMAVMATYLMQEHVDTCKRKTKAS 128
DB 69 LSVINLDEINPEGFCILDFMTYSRLNREGNIMAVMATYLMQEHVDTCKRKTKAS 128
QY 129 EAMWSAIPREPEFLNSRMLMPODIMAYRGREVENNIPLSAPGCEERAP 184
DB 129 EAMWSAIPREPEFLNSRMLMPODIMAYRGREVENNIPLSAPGCEERAP 184
QY 185 YS-----GLSTP--PASYSVSHLPVSSLLFSDSEFSDVMPVAPNPPKERRALPCDSARP 237
DB 185 YS-----GLSTP--PASYSVSHLPVSSLLFSDSEFSDVMPVAPNPPKERRALPCDSARP 237
QY 238 VPGEYSRPTLEVPNVCHSNISPKETIPREASDMHYSAEGLKPAAPARNAAPYPCD 297
DB 238 VPGEYSRPTLEVPNVCHSNISPKETIPREASDMHYSAEGLKPAAPARNAAPYPCD 297
QY 298 KASKEERPSSEDEIALHFEPPNAPLNKGLVSPQSPQSDCOPNSTEACSSKNACI 355
DB 298 KASKEERPSSEDEIALHFEPPNAPLNKGLVSPQSPQSDCOPNSTEACSSKNACI 355
QY 356 LQASG--SPPAKSPTDPPKACMKKKYKFTVLSNLQNAKPGGPEQAEIGRLSPRAY 406
DB 356 LQASG--SPPAKSPTDPPKACMKKKYKFTVLSNLQNAKPGGPEQAEIGRLSPRAY 406
QY 407 AYTAAPACOPMPERENLQSPTKLSASGSDSTIPQASRLNNIVNRSMTGSPRSSSESHS 466
DB 407 AYTAAPACOPMPERENLQSPTKLSASGSDSTIPQASRLNNIVNRSMTGSPRSSSESHS 466
QY 467 PLY-----MH-----PPKCTSGSGSPQHAEWCLHTAGPTFAEWEGETOSEYSDS 511
DB 467 PLY-----MH-----PPKCTSGSGSPQHAEWCLHTAGPTFAEWEGETOSEYSDS 511
QY 512 SCE-----NGAFCNECDRCRSEASLKRHTLOTSH--DKPYKCDRCQ 552
DB 512 SCE-----NGAFCNECDRCRSEASLKRHTLOTSH--DKPYKCDRCQ 552
QY 552 HCDKKFQVGNLKAHLKIHIADGPKCRBECKOPTTSGNLKRO--LRHSGEKPYVCIHQ 508
DB 552 HCDKKFQVGNLKAHLKIHIADGPKCRBECKOPTTSGNLKRO--LRHSGEKPYVCIHQ 508

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/761,117
FILING DATE: 16-Jan-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/43771-A-PCT-US-Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-761-117-9

Query Match 14.8%; Score 560; DB 2; Length 110;
Best Local Similarity 99.1%; Pred. No. 6.3e-43;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 CIOETRASDVLTNLRSLDITDVIVVSRQFRAHKTVMACSGLFYSITDOLK 67
1 CIOETRASDVLTNLRSLDITDVIVVSRQFRAHKTVMACSGLFYSITDOLK 60

Qy 68 NLSTVINDPEINPEGFCILDFMTSLRLREGNIMAVMATVLMQEHV 117
61 NLSTVINDPEINPEGFCILDFMTSLRLREGNIMAVMATVLMQEHV 110

Db 61 NLSTVINDPEINPEGFCILDFMTSLRLREGNIMAVMATVLMQEHV 110

RESULT 11
US-09-949-016-7651
Sequence 7651, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7651
LENGTH: 733
TYPE: PRT
ORGANISM: Human
US-09-949-016-7651

Query Match 14.2%; Score 540; DB 2; Length 733;
Best Local Similarity 25.0%; Pred. No. 8e-40;
Matches 190; Conservative 103; Mismatches 270; Indels 196; Gaps 29;

Qy 11 FTRNASDVLTNLRSLDITDVIVVSRQFRAHKTVMACSGLFYSITDOLK 70
50 FTRNASDVLTNLRSLDITDVIVVSRQFRAHKTVMACSGLFYSITDOLK 108

Db 50 FTRNASDVLTNLRSLDITDVIVVSRQFRAHKTVMACSGLFYSITDOLK 108

Qy 71 VINDPETINPEGFCILDFMTSLRLREGNIMAVMATVLMQEHV 126
109 VINDPETINPEGFCILDFMTSLRLREGNIMAVMATVLMQEHV 159

127 ASRAENVSAIKPREEFLNSRLMPQDIMAYRGREVENNLPLRSAPGESRAFAFSLYS 186
160 -----KP-----KTSVGOAAGQ-----S 173

Qy 187 GLSTPPASYSMTYSHLPSLSDEEFDVMEVNPFPKRALPCDSAPVPGESRPT 246
174 GLG-PPASQVNSHVKEPAGLEEEVSRTGL-----VPRDQ-PRGSHSP-----ORPQ 221

Qy 247 LEVSPVNCNSNIYSPKETTPEEKASDMYVAGLCPA-----APBARNAFPPOCKASK 301
222 L-----HSPAQS-----EGPSSLCGKLKQALPCPLEDKRPBDCRVPPLLEBGA 267

Qy 302 EEPSPSEDEIALHFE-----PNAPLNKGVLSPQSPKSCQPNSPPEACSSKN 352
268 QLOGSSNEVEVQVEDDGDGYMSPEAVLTR-----KSNVIRKPCAAB 314

Qy 353 ACILQASGSPPAKS-----PTDPAKCNMK-----KYRETVLSLNQNAKPGAPQABIGRL 403
315 ALSAGSLAEPALNRKGTAVPVBCPTCHKKFLSKYLLKVNRRKHTEKEP----- 363

Qy 404 SPRAYTAPACQOPMEPENIDLOSPTKLSASGEDSTTPQASRLNNTVNRG--MTGSP-- 458
364 -----FPCPKGCKCYFRKENT-----LEHEAR--NCMNRSEOVFTCSVCVQ 401

Qy 459 -----RSSSESHSPLYMT-----PPKCTSCGSGSPQHAEMCLHT-----AGPTFAE-E 500
402 ETRFRMRNLRVHVSHTEGMEPYRSCSQOPWCKKQDQSMITLHGAPKPAHACPTCAKCF 461

Qy 501 MGEIOSESPSCENG--AFPCNECDRFESEASLKRHTLQTH-SDPYKCDRCQASFRY 557
462 LSTETDLMHAFKRGKEKLFVCEECHRASRNGLOMHTAKRNRBPHCECSNAFTQ 521

Qy 558 KGNLASHKTVHTEKEPYRNCICGAOPNRPANLKTHTRISGEKPYKCEITCGARFVQYAH 617
522 KANLNMHLRHTGEKPEQCHLCKTFRTOASLDKRNRTHTGERPFCEORFTEKGPL 581

Qy 618 RAYVLI-HTGEKPYCEICGTRPRHLQTLKSHLRHTGEKPYKCEITCGARFVQYAH 676
582 LRHVASHRQBRPHFCQICGTEKFAVEQQLVHVRHRHGVKFCCTEGYKFPQAHLLRH 641

Qy 677 LRQKGAITNTKYQYR-----VSATDLPPEL 702
642 M-ELHREVENYNPQRKLRNLIIEDKAMVVVALQPPAEL 679

Db 677 LRQKGAITNTKYQYR-----VSATDLPPEL 702
642 M-ELHREVENYNPQRKLRNLIIEDKAMVVVALQPPAEL 679

RESULT 12
US-08-340-203A-10
Sequence 10, Application US/08340203A
Patent No. 5756668
GENERAL INFORMATION:
APPLICANT: Baylin, Stephen B.
APPLICANT: Wales, Michele M.
TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE, HIC-1
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: California
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,203A
FILING DATE: 15-NOV-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.

REGISTRATION NUMBER: P-38,347
REFERENCE/DOCKET NUMBER: 07265/039001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-340-203A-10

Query Match 14.2%; Score 538; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 5.9e-41;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TRHSDVLTNLRSRDILTDVIVVSRQFRAKTVLMACSGLFYSIFTDLKCNLSV 71
DB 1 TRHSDVLTNLRSRDILTDVIVVSRQFRAKTVLMACSGLFYSIFTDLKCNLSV 60
QY 72 INLDPEINPEGFCILLDFMTSRLNLRGNIMAVMATMYLQMEHV 117
DB 61 INLDPEINPEGFCILLDFMTSRLNLRGNIMAVMATMYLQMEHV 106

RESULT 13
US-08-452-427-10
Sequence 10, Application US/08452427
Patent No. 5922590
GENERAL INFORMATION:
APPLICANT: Baylin, Stephen B.
APPLICANT: Wales, Michele M.
TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE, HIC-1
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: California
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,427
FILING DATE: 26-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/340,203
FILING DATE: 15-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Halie, Ph.D., Lisa A.
REGISTRATION NUMBER: P-38,347
REFERENCE/DOCKET NUMBER: 07265/039001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-452-427-10

Query Match 14.2%; Score 538; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 5.9e-41;

Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TRHSDVLTNLRSRDILTDVIVVSRQFRAKTVLMACSGLFYSIFTDLKCNLSV 71
DB 1 TRHSDVLTNLRSRDILTDVIVVSRQFRAKTVLMACSGLFYSIFTDLKCNLSV 60
QY 72 INLDPEINPEGFCILLDFMTSRLNLRGNIMAVMATMYLQMEHV 117
DB 61 INLDPEINPEGFCILLDFMTSRLNLRGNIMAVMATMYLQMEHV 106

RESULT 14
US-09-085-407-10
Sequence 10, Application US/09085407
Patent No. 6103877

GENERAL INFORMATION:
APPLICANT: Baylin, Stephen B.
APPLICANT: Wales, Michele M.
TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE, HIC-1
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: California
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/085,407
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/340,203
FILING DATE: 15-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Halie, Ph.D., Lisa A.
REGISTRATION NUMBER: P-38,347
REFERENCE/DOCKET NUMBER: 07265/039001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS: No. 6103877 Relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-085-407-10

Query Match 14.2%; Score 538; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 5.9e-41;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TRHSDVLTNLRSRDILTDVIVVSRQFRAKTVLMACSGLFYSIFTDLKCNLSV 71
DB 1 TRHSDVLTNLRSRDILTDVIVVSRQFRAKTVLMACSGLFYSIFTDLKCNLSV 60
QY 72 INLDPEINPEGFCILLDFMTSRLNLRGNIMAVMATMYLQMEHV 117
DB 61 INLDPEINPEGFCILLDFMTSRLNLRGNIMAVMATMYLQMEHV 106

RESULT 15
US-09-949-016-10273
Sequence 10273, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307
 CURRENT APPLICATION NUMBER: US/09/949,016
 PRIOR FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 10273
 LENGTH: 678
 TYPE: PRT
 ORGANISM: Human
 US-09-949-016-10273

Query Match 13.4%; Score 508; DB 2; Length 678;
 Best Local Similarity 26.0%; Pred. No. 5.6e-37;
 Matches 187; Conservative 102; Mismatches 285; Indels 144; Gaps 27;

9 IOTFRASDVLLINLRSLDILTDVIVYVSRQFRAKTYLMACSLFYSIFTDQKCN 68
 16 LQNPSPHTGLCKANQRLAGTLCVIVIMVDSQFHAHRTVLAQTSKMFELF---HRN 71
 69 LSVINILPEINBEFCILLDFMTSRNLREGNIMAVMATAMYLOMEHVVDTCRPIKA- 127
 72 SQHYTLDFLSPKTFQOLEYATYATLOAKAEDLDLLYABEILEIYEBQCLMLETI 130
 128 -----SEAEMVSAIKPREEPFLNSRLMPODIMAYRGREVENNLPLRSAPG-CESRA 179
 131 QASDNDTEATMDG-GAEBEDKAKYIKNIIFISKSSSESGYASVAGSLPGPMWDQS 189
 180 PABSLYGLST-PPASTSMYSHLFVSSLFSDSEFRDVRMPVANPPKERALPCDSARPV 238
 190 PSVSTSPGLSMTSPTKAADVSLMTIGQSL-----LQGTLOPPAG-PEEPTLAGGGRHPG 242
 239 PGEYSRPTLEVSPPVCHSNISYSPKETIPEEASDMHYVAGLKPAAASANNAPYPPDX 298
 243 VAETKTEMQVDE-----VPSQDSPGAES-----SISGM----- 273
 299 ASKEERPSSEDEIALHFEPPNAPLNKGLVSPQ-----SPQSDQPNSPTEACSSXNAC 354
 274 GDKYBERGK-----EGRGTPTRSSVITSARELHYGRESABQVPPPAEA----- 317
 355 ILQASGSPPAKSPDPAKCMKKYKFIVLNSLNONAKPGGEQAELEGRLSPRAYTADPPAC 414
 318 -----GQAPTRPRHPAP-----PREKHGIYSVLPNHK-----ADAVLSMPSVTSGLHV 363
 415 QPPEPERLDQSTPKLSAGEDST---IPQA-----SRANNIVRSMTGSPRSSSE 463
 364 QP-----ALAVSMDFTSYGGLPQGTQRELFKLGELA-VGKKSSERTIGE 409
 464 SHSPLVMHPKCTSGSOSP-----QHAEMCLHTAGPTFAEMGETOSEYSDS----- 511
 410 -----QCSVCGVELPNEAVEQHRK--LHSGMKTTCYCEL--CGKRLDLSRLRMH 455
 512 -----SCENGAPFCNECDRCFSEASLKRHTLQTH--SDKPYKCDRCQASFRYKGNLASHK 565
 456 LLAHSAGAKAFVDCQCGAOFKEDALETHR-QTHGTDMAVFCLCGKRFQASALQOHM 514
 566 TVHTGKPYRCNICGAQPNRPANLKTHTIRISGKPYKCTCGARFVQVAHLRAVLIHT 625
 515 EVHAGVRSYISCEKRTTPSHLTALKRHLRSHTGHPYECFCGSCFRDESTLKSRIHT 574
 626 GEKPYPCBICGTRFHLQTLKSLRIHTGKPYKCEKCNLAFRRHKSQRLRLRQKGA 683
 575 GEKPYECGCGKSLKQLTETHYRVHTGKPYFECKLCHQSRSDYSAMIKHLRTNKA 632

Search completed: March 2, 2006, 03:55:22
 Job time : 49 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 2, 2006, 04:07:37 ; Search time 21 Seconds
(without alignments)
672.386 Million cell updates/sec

Title: US-10-755-889-18

Perfect score: 3793
Sequence: 1 MSPADSCIOFTTHASDVLL.....TKVQYNSATDLPPELPKAC 706

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 135339 seqs, 20000136 residues

Total number of hits satisfying chosen parameters: 135339

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

Published Applications_AA_New:*
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8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	503	13.3	799	US-11-072-512-2929	Sequence 2929, Ap
2	469	12.4	541	US-11-072-512-2161	Sequence 2161, Ap
3	468.5	12.4	540	US-11-072-512-3748	Sequence 3748, Ap
4	465.5	12.3	781	US-11-072-512-2937	Sequence 2937, Ap
5	465	12.3	586	US-11-072-512-2592	Sequence 2592, Ap
6	463	12.2	556	US-11-072-512-3914	Sequence 3914, Ap
7	458.5	12.1	530	US-11-072-512-2805	Sequence 2805, Ap
8	458	12.1	530	US-11-072-512-3434	Sequence 3434, Ap
9	457	12.0	409	US-11-072-512-2663	Sequence 2663, Ap
10	457	12.0	475	US-11-072-512-3470	Sequence 3470, Ap
11	455	12.0	429	US-11-072-512-2786	Sequence 2786, Ap
12	454.5	12.0	504	US-11-072-512-2053	Sequence 2053, Ap
13	454	12.0	636	US-11-072-512-2449	Sequence 2449, Ap
14	452	11.9	500	US-10-517-151-4	Sequence 4, App11
15	445	11.7	643	US-11-072-512-2241	Sequence 2241, Ap
16	442.5	11.7	592	US-11-072-512-3366	Sequence 3366, Ap
17	442	11.7	543	US-11-072-512-3461	Sequence 3461, Ap
18	440	11.6	334	US-11-072-512-2450	Sequence 2450, Ap
19	435	11.5	577	US-11-072-512-2569	Sequence 2569, Ap
20	434.5	11.5	1024	US-10-330-773-927	Sequence 927, App
21	433	11.4	575	US-11-072-512-3423	Sequence 3423, App
22	432.5	11.4	553	US-11-072-512-3306	Sequence 3306, Ap
23	432	11.3	816	US-11-072-512-2341	Sequence 2341, Ap
24	430.5	11.3	487	US-11-072-512-2868	Sequence 2868, Ap
25	428	11.3	407	US-11-072-512-3895	Sequence 3895, Ap

26	426.5	11.2	357	7	US-11-072-512-2570	Sequence 2570, Ap
27	425.5	11.2	526	7	US-11-072-512-3582	Sequence 3582, Ap
28	425.5	11.2	732	7	US-11-072-512-3474	Sequence 3474, Ap
29	424.5	11.2	350	7	US-11-072-512-2500	Sequence 2500, Ap
30	423.5	11.2	231	7	US-11-072-512-3821	Sequence 3821, Ap
31	423.5	11.2	487	7	US-11-072-512-3571	Sequence 3571, Ap
32	421.5	11.1	467	7	US-11-072-512-3083	Sequence 3083, Ap
33	421.5	11.1	498	7	US-11-072-512-2548	Sequence 2548, Ap
34	420	11.1	365	7	US-11-072-512-3671	Sequence 3671, Ap
35	419.5	11.1	437	7	US-11-072-512-2932	Sequence 2932, Ap
36	417.5	11.0	432	7	US-11-000-463-365	Sequence 365, Appl
37	415	10.9	720	7	US-11-121-438-18	Sequence 18, Appl
38	410.5	10.8	689	7	US-11-121-438-2	Sequence 2, Appl
39	409	10.8	465	7	US-11-072-512-2590	Sequence 2590, Appl
40	407.5	10.7	641	7	US-11-072-512-2385	Sequence 2385, Appl
41	406.5	10.7	1011	6	US-10-330-773-924	Sequence 924, Appl
42	405	10.7	494	7	US-11-072-175-181	Sequence 181, Appl
43	399.5	10.5	307	7	US-11-072-512-2986	Sequence 2986, Appl
44	399	10.5	302	7	US-11-072-512-2998	Sequence 2998, Appl
45	394	10.4	172	6	US-10-888-613B-75	Sequence 75, Appl

ALIGNMENTS

RESULT 1
US-11-072-512-2929
Sequence 2929, Application US/11072512
Publication No. US20060029945A1
GENERAL INFORMATION:
APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHITO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OR INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072.512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2929
LENGTH: 799
TYPE: PRT
ORGANISM: Homo sapiens
US-11-072-512-2929
Query Match 13.3%, Score 503, DB 7, Length 799;
Best Local Similarity 24.3%, Pred. No. 5.7e-29;
Matches 186; Conservative 86; Mismatches 270; Indels 224; Gaps 32;
QY DVTIVSREQFRKHTVIMACGLFYSIFTDQKCNLSVINLDEINDEGCILLDFEY 92
DB DVAVVFSREBR---LIDTQKRLYRDVWENFR-NIVAVGHLF-FQPD-----MV 72
QY 93 SKLVLRGNTMAVWATMYLQMEHVVDTCRFL-----KASEAEVNSAIK 137

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Db      73  S Q L E A E K L M M W E T E T O R S S K H N K M E T I O K F A L K T L S N O E L S C W Q I W Q V A S E L R C Q 132
Qy      138  P P R E E F L ----- N S R M L M P O D I M A Y ----- R G 159
Db      133  G K S S Q L O Q D S I Q V S E N N E N N I M P K D S S I Y I E N O E P W R T O H S C G N T Y L S E S Q I O S R G 192
Qy      160  R E V - V E N N I P ----- L R S A P G C E S R A F A P S I V S G L S T P P A S V S M Y S H L V S L L P S D E F 213
Db      193  K Q I D V A N N I Q I H E D E F M K S P ----- F H E H I K T D T E P K C K G E Y G K ----- I I S D G S - 239
Qy      214  R D V R M F V A N P P K E R A L P C D S A R P V G E Y S R ----- P T L E V S P N V ----- C --- H S N I Y S 260
Db      240  - N Q K L P L G ----- E K H P C ----- G E G R G F S Y S P R L P I H V N H T G E K C F S Q S S H L R T 286
Qy      261  P R E T T I E E A R S D M H Y V A E G L K P A A P S A R N --- A P Y P C D K A S K E E R P S S E D E I A L H P 316
Db      287  H O R I H G E K L M R C H E S G D C F N K S S F H S Y O S N H T G E K S Y C D S C G K F --- S S S T G L I I H Y 343
Qy      317  E P P N A P L N K G L V S P O S P O K S D C Q P N S P T E A C S S K N A C L I O A S G S P A K S P T D P K A C M K 376
Db      344  R H T H G ----- E K P Y K ----- C E C K C F S Q S S ----- 365
Qy      377  K Y K F I V L N S I N O N A K E G S E O A E L G ----- R L S P R A Y T A P P A C O P M E P E N L D I Q S P T 429
Db      366  - - N F O G H Q V H T E K Y K C E C G K G F G W S V N L V H Q R V H R G ----- E K P Y 408
Qy      430  K I S A S E D S T I P O A S R L N N I V N S M T G S P R S S E ----- S H - S P L Y M H ----- P R K 474
Db      409  K C E C K G K F T - - O A A H F - H I H Q R V H T G E K P Y K C D V C G K G F S H N S P I C H R R V H T G E K P Y K 465
Qy      475  C T S C G S Q S P O H A M C L H T A G P T A E M G E T O S E Y S D S C E N G ----- 516
Db      466  C R A C G K F T N T L D L H N ----- F R V H T G E - - K P Y K C E C G K G F S Q A S N I Q V H O N V H T G E K 518
Qy      517  A P F C N E C D C R F S E A S I K R H T L Q T H S D K P Y C D R C O A S F R Y K G N L A S H K T V H T G E K P Y K 576
Db      519  R F C E T C G K G F S S L Q T H Q R V H T G E K P Y C D V C G K D P F S Y S N L K H Q V I H T G E K P Y K 578
Qy      577  N I G A O P N R P A N I K T T R I H S G E K P Y K C E T C G A R F V Q A H L R A V L I H T G E K P Y P E I G 636
Db      579  E E C G K F S W S N S L A H O R V H S G E K P Y K C E C D C S F S Q A I D F R V H O R V H T G E K P Y K G V G 638
Qy      637  T R F R H I Q T L K S H I R H T G E K P Y C E K C N L F R H K S Q L R L R O K G 682
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RESULT 2

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US-11-072-512-2161
; Sequence 2161, Application US/11072512
; Publication No. US2006002945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHITO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTUKU
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191

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; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2161
; LENGTH: 541
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2161

```

Query Match 12.4%; Score 469; DB 7; Length 541;

Best Local Similarity 28.6%; Pred. No. 1e-26; Indels 134; Gaps 26;

Matches 153; Conservative 60; Mismatches 188; Indels 134; Gaps 26;

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Qy      216  V M P V A N P P K E R A L P C D S A R P V G E Y S R P T L E V S P N V C H S N I Y A P K E T I P E A R S D M H Y 275
Db      3  L K M T T R N - F P - B R E V P C D V ----- E V E R F T R E V P --- C L S L G D G W M D C - E N O G C H L R Q 49
Qy      276  S V A E G L K P A A P S A R N A P Y P C D K A S K E E R P S S E D E I A L H P P N A P L N R K G L V S P O S Q 335
Db      50  S A L T L E K P E T O R A ----- I C E Y P G F G H L I A S S D ----- L P P S O R V I A T N G F A P D S N V 98
Qy      336  K S - D C Q P N S P T ----- E A C S S K N A C ----- I I Q A S G --- S P P A K S P T D P K A C M K 375
Db      99  S G L D C D P A L P S Y P K S Y A D R T G D S D A C G K G F N S H E V I A H G R N P V R E K Y K I P E S Y A S F M H 158
Qy      376  ----- K K Y K ----- F I V L N S I N O N A K - P G A P R O - A E I G R ----- 402
Db      159  F T S L G H Q K I M R G K G S Y E K N K E N I F T L S S I N E Q R N L P G K Q Y R C T E C G C F P R N S S L 218
Qy      403  - L S P R A Y T A - P P A C O P - P M E P E N L D L ----- O S P T L S A S G ----- E D S T I P O A S 444
Db      219  V L H R H T H T G E K P Y T C N E C G S F S K N Y N L I V H O R I H T G E K P Y C S K G A F S D S A L T O H Q 278
Qy      445  R L N N I V N S M T G S P R S S S H S P L V M H P P K C T S C G S Q S P O H A M C L H T A G P T A E M G E T 504
Db      279  R I H ----- T G E ----- K P Y C L E C G T F R N S S L I L H O R T H T ----- G E K 313
Qy      505  Q S E Y S D S C E N G A F P C N E C D C R F S E A S I K R H T L Q T H S - D K P Y C D R C O A S F R Y K G N L A S 563
Db      314  ----- P Y C N E C G K F T D I S H L T V A - L A I H T G E K Y E C S K G K A R D S S Y L N Q 360
Qy      564  H K T V H T G E K P Y C N I C G A O F N R P A N I K T T R I H S G E K P Y K C E T C G A R F V Q A H L R A V L I 623
Db      361  H E R T H T G E K P F E C A C G K S F N N S H L I V H O K I H S G E K P E C K E C G K T F E S A Y L I R H O R I 420
Qy      624  H T G E K P Y P E I C G T F R H I Q T L K S H I R H T G E K P Y C E K C N L F R H K S Q L R L R O K G 678
Db      421  H T G E K P Y G N O C Q L F R N I A G L I R H O R T H T G E K P E C N O C G A F R D S S C L T Y H O R 475

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RESULT 3

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US-11-072-512-3748
; Sequence 3748, Application US/11072512
; Publication No. US2006002945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO

```

APPLICANT: SEKI, NAOHITO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOTYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3748
LENGTH: 540
TYPE: PRT
ORGANISM: Homo sapiens
US-11-072-512-3748

Query Match 12.4%; Score 468.5; DB 7; Length 540;
Best Local Similarity 37.3%; Pred. No. 1,1e-26;
Matches 91; Conservative 27; Mismatches 87; Indels 39; Gaps 4;

QY 472 PPKTSCGSGSPQHAEMCLHT---AGPTFAEEMGE--TQSE-----YSD 510
DB 255 PYKCECGKAFNPFNLTKHKIHTGBOPIYCECECKAFQSSSTLTKHKIHTGKPYKC 314
QY 511 SSCENG-----APFCNCCDRPSEASLKRHTLQTHSDKPYKCDRCQ 552
DB 315 BECGKAFNRSSKLTGKHNHTGBOPIYKCECGKAFNRSSNLTKHKIHTGKPYKCEG 374
QY 553 ASFRYGNLASHKTVHTGKPYRCNCGAOFNRPANLKTHTRIHSGKPYKCECGARFV 612
DB 375 KAKHSSALTKHRIHTGKPYKCECGKAFNRSSKLTGKHNHTGKPYKCECGARFV 434
QY 613 QVAHLRAHVLHTGKPYPCICGTRFRHLQTLKSHRIHTGKPYKCECNLHFRHSQ 672
DB 435 QSSKLTGKHNHTGKPYKCECGKAFNRSSSLTKHRIHTGKPYKCECGARFV 494

QY 673 LRLH 676
DB 495 LTEH 498

RESULT 4

US-11-072-512-2937
Sequence 2937, Application US/11072512
Publication No. US20060029945A1
GENERAL INFORMATION:
APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHITO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOTYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07

PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2937
LENGTH: 781
TYPE: PRT
ORGANISM: Homo sapiens
US-11-072-512-2937

Query Match 12.3%; Score 465.5; DB 7; Length 781;
Best Local Similarity 38.4%; Pred. No. 2.9e-26;
Matches 93; Conservative 29; Mismatches 91; Indels 29; Gaps 5;

QY 465 HSPLYMH-----PPKTSQSGSPQHAEMCLHT---AGPTFAEEMGETQSYSDS 511
DB 477 HSRLLAHQRHTGKPYKCNBCKGVFSQHSRLAVHRIHTGKPYKCKEKGKV---FSDR 533
QY 512 SC-----ENGAFPCNCCDRPSEASLKRHTLQTHSDKPYKCDRCQASFRYGNLA 562
DB 534 SAPARRHRIHTGKPYKCKEKGKVFSQCSRLTVHRRHISGKPYKCNBCKGVFSQYSHLV 593
QY 563 SHKTVHTGKPYRCNCGAOFNRPANLKTHTRIHSGKPYKCECGARFVQVAHLRAHVL 622
DB 594 GHRVHTGKPYKCECGKAFNRSSNLTKHKIHTGBOPIYKCECGKAFNRSSNLTKHKIHTG 653
QY 623 IHTGKPYPCICGTRFRHLQTLKSHRIHTGKPYKCECNLHFRHSQ 678
DB 654 VHTGDRPYKCNBCKGVFSQCSRLTVHRRHISGKPYKCNBCKGVFSQYSHLV 713
QY 679 QK 680
DB 714 EK 715

RESULT 5

US-11-072-512-2592
Sequence 2592, Application US/11072512
Publication No. US20060029945A1

GENERAL INFORMATION:

APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHITO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOTYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2592
LENGTH: 586
TYPE: PRT

ORGANISM: Homo sapiens
US-11-072-512-2592

Query Match 12.3%; Score 465; DB 7; Length 586;
Best Local Similarity 37.8%; Pred. No. 2.2e-26;
Matches 98; Conservative 31; Mismatches 106; Indels 24; Gaps 4;

QY 472 PKCTSGSGSPQHAE-----CLHTA-GPTFAEMGB-----TQSEYSDSCENGAFFC 520
DB 228 PTKCECGCAFNSSULTGKIIHTGEKPYKCECGKAFNBSSTLTGKRIHTGEKPYK 287
QY 521 NECDRFSSEASLKRHTLTQTHSDPKYCDRCQAFRYKGNLASHKTVHTGEKPYRNCIG 580
DB 288 EBCGKAFNQSILNKRIHMDKPYKCECGKAFNVSILKKKIIHTGEKPYKCECG 347
QY 581 AQPNRPANIKTRIRHSGEKPYKCECGKAFNVAHLRAHVLHTGEKPYPCICGTRR 640
DB 348 KAFNPSNLTGKIIHTGEKPYKCECGKAFNQSSTLTGKRIHTGEKPYKCECGKAFK 407
QY 641 HQTLSKSHLRHTGEKPYKCECGKAFNRSQSLRLRLRO-----KHGATWT 687
DB 408 QGSTLTREKIIHTGEKPYKCECGKAFNVSATFTKHKHMDKPYKCECGKAFSVST 467
QY 688 KQYRVASATDLPPELPKAC 706
DB 468 LTKHKIIHTRKPYKCECG 486

RESULT 6

US-11-072-512-3914
Sequence 3914, Application US/11072512
Publication No. US20060029945A1
GENERAL INFORMATION:

APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHITO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOKYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3914
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapiens
US-11-072-512-3914

Query Match 12.2%; Score 463; DB 7; Length 556;
Best Local Similarity 26.7%; Pred. No. 2.9e-26;
Matches 156; Conservative 76; Mismatches 218; Indels 134; Gaps 22;
147 RMLPDDIMAYRREVENN-LPLR-----SAPCESRAFAPSLVSGLSTPPASYSYMSH 200

DB 42 RVVLPVPTLGRNPVARDASAVPARDPAMLQEDKVEERANAPGLPTACSOBPVTFAV-- 99
QY 201 LPVSLFSDE-----PRDVM-----PVANPPKRALPCGSARPVPEY 242
DB 100 ---AVVTFPEBWVFLDSTQSLRVDVNLVNTYRNLAASVADOLCKNALSTYLER---GEO 152
QY 243 SRPTLEVPNVCHSNIVSPKETIPEARSIMHYV-ABGLPRAAPSARNAPFPCKASK 301
DB 153 WTTORGLVLDPCABRQCQPGALPQDFTTEILSIDVGBQO-----PCKLYK 202
QY 302 --EERPSSEBIALHFPNPAPLNRKGLVSPQSKDDCPNBPTEACSSGNACILQAS 359
DB 203 YNRLEKPNNSIEPLRQYRIHA-----GASCEQ-----EIRNSFFQSAH 243
QY 360 GSPPAKSPTDPK--ACMKKKYFIVLNGLANAKPGGEQA---ELG-----RLS 404
DB 244 LIVPEKISGDKSYACNCKEFSRYSSDLIRHKTHTKEKCDQCECGKAFYSSNLRRH 303
QY 405 PRAYTAPPAQCPMPEBNIDLQSPYKLSASGEDSTIPQASRLNIV--NRSMTGSPRSS 462
DB 304 MRTHTG-----EKPECGCGKFTF-----RNFNLILHQRNHTG----- 338
QY 463 BSHSPLVNHPPKCTSGSOSPOHAEMLCHTAGPTFAEMGETQSEYSDSCENGAFFCNE 522
DB 339 -----KPYECKDCGKAFNQPSSLSRSHVTRHT-----GEX-----PFECSQ 373
QY 523 CDCRFSSEASLKRHTLTQTHS--DKPYKCDRCQAFRYKGNLASHKTVHTGEKPYRNCIGA 581
DB 374 CGKAFREHSSLTTH--LRHTTREKPYECNOCKKFPFTSHLNVHKAIRYGEKLYECATCQ 432
QY 582 QPNRPANIKTRIRHSGEKPYKCECGKAFNVAHLRAHVLHTGEKPYPCICGTRPRH 641
DB 433 VLSRLSTLSKSHRHTHTGEKPYKCECGKAFNVSATFTKHKHMDKPYKCECGKAFSVST 492
QY 642 LQTLKSHLRHTGEKPYKCECGKAFNRSQSLRLRLROKHGATWT 685
DB 493 SSSLIVHVRTHSAGRPOCNOCEKAFRHSSTLTGKRIHTGEKPYKCECGKAFSVST 536

RESULT 7

US-11-072-512-2805
Sequence 2805, Application US/11072512
Publication No. US20060029945A1
GENERAL INFORMATION:

APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHITO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOKYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2805

```

; LENGTH: 561
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2805

```

Query Match	12.1%;	Score 458.5;	DB 7;	Length 561;
Best Local Similarity.	30.6%;	Pred. No. 6.3e-26;		
Matches 138;	Conservative 47;	Mismatches 167;	Indels 99;	Gaps 18;

QY	302	EEEPSSSDEIALHEPPNAPLNKGLVSPQSDOPNSPTACSSKACIALQASG	361
Db	70	EEKPSSQ-----HELINTSRNYSIMKFMENKSGKC-----FCDEKHHI-----	111
QY	362	PPANSPTDPKACNMKKYFYIVINSINQAKPGCPQA-----ELGRLSP-----RAY	408
Db	112	---HSEEPSEYNKNGNSFWINMEDLIWOKIKMWEOSFEYNCGKAFPENSLFLVHKGY	168
QY	409	TAPRACO-----PME-----PEN-----LDLOSPTLSASG	435
Db	169	TGQCTCKTTEHGKTCDSMFFTHQOHTPRENHYGECGBENIPEBSILLEHQSVPFSQKL	228
QY	436	EDSTIPOASRLNNIVNRSMTGSPRSSBSHSLPYNH-----PCKTSG-----SQS	482
Db	229	NULPIQRTHSINNILLIENYECGTFSEK-----LVHLAQOHTTGEKPEYECHECGKTFYOK	283
QY	483	POHA-EMCLHTNG-PTFAEMETOSYSVD-----SSCENG--AFPCNEDCRESBASLK	534
Db	284	SANTHROHTTGEKPEYECHECGKTYKNSDILKHORINTGERPYCNEHGKSFSEKSTLT	343
QY	535	RHTLOTHS-DKPYKCDROCAFPRYKGNLASHKTVTGEKPYRCNICGAQPNRPANILKTHT	593
Db	344	OHQ-RHTHGEKPEYECHECGKTFSPKSVLTVHQKHTTGEKPYRCVACGKAFKASDLINQ	402
QY	594	RHSGEKPYKCESTCGARFVQVAHLBAVLIHTGEKPYRCEICGTRPHILOTLKSHLRHT	653
Db	403	RHTHGEKPEYECHECGKSFSEKSTLTVHILHTHTEKPYECIOCGKFFCYVSGTEHLRRT	462
QY	654	GEKPYHCEKCNLHFRHKSOL-----RYLHROK	680
Db	463	GEKPYHCEKCGKTFROKSLIYNORTHROK	493

RESULT 8
US-11-072-512-3434
Sequence 3434, Application US/11072512
Publication No. US20060029945A1
GENERAL INFORMATION:
APPLICANT: ISOGAI, TARAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: MAKAMATSU AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YURIKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHKO
APPLICANT: YOSHIKAWA, TOSYOMU
APPLICANT: OTSUKA, MOTOTYKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cdna
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072, 512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350, 978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP. 2001-379258
PRIOR FILING DATE: 2001-11-05

```

; NUMBER OF SEQ IDNOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3434
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3434

```

Query Match	12.1%;	Score 458;	DB 7;	Length 530;
Best Local Similarity	39.0%;	Pred. No. 6.4e-26;		
Matches 94;	Conservative 27;	Mismatches 88;	Indels 32;	Gaps 4

[illegible]

```

RESULT 9
US-11-072-512-2663
; Sequence 2663, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHITO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTYOUKI
; APPLICANT: NAGAHARA, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 08435-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2663
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2663
Query Match      12.0%  Score 457,  DB 7,  Length 409,

```

[illegible]

Db	192	HIGKSEJVECKEC--GKFFSCGSHVTRLKLIHTEGKEPFECKECGKAFSCSSILSHQRIHT	249
Qy	542	SDKRYKCDRCQASFRYKGNLASHKTVTGTGEKPYRCNICGAQFNRPANLKTHTRIHSGEKP	601
Db	250	GKKRYECKEGCKAPKAFVSCSNLIDHQRIHTEGKEPYECKYCKGKAFKXSOLFOHARIHTEGKP	309
Qy	602	YKCTCGARFVQVNLHAAVLIHTEGKEPYCEICGTFRHLQTLKSHLRIHTEGKPYNCE	661
Db	310	YECKECKKAFQSSSKLVQHQRIHTEGKEPYECKGCKAFSSGSAALTNHQRIHTEGKEPYDCK	369
Qy	662	KCNLHPRKNSQLRLHLR	678
Db	370	ECGKAFQSSQLRQHQR	386
RESULT 11			
US-11-072-512-2786			
Sequence 2786, Application US/11072512			
Publication No. US20060029945A1			
GENERAL INFORMATION:			
APPLICANT: ISOGAI, TAKAO			
APPLICANT: SUGIYAMA, TOMOYASU			
APPLICANT: OTSUKI, TETSUJI			
APPLICANT: MAKAMATSU, AI			
APPLICANT: SATO, HIROYUKI			
APPLICANT: ISHII, SHIZUKO			
APPLICANT: YAMAMOTO, JUN-ICHI			
APPLICANT: ISONO, YUUKO			
APPLICANT: HIO, YURI			
APPLICANT: OTSUKA, KAORU			
APPLICANT: NAGAI, KEIICHI			
APPLICANT: IRIE, RYOTARO			
APPLICANT: TAMECHIKA, ICHIRO			
APPLICANT: SEKI, NAOHICO			
APPLICANT: YOSHIKAWA, TSUTOMU			
APPLICANT: OTSUKA, MOTOUKI			
APPLICANT: NAGAHARI, KENJI			
APPLICANT: MASUHO, YASUHIKO			
TITLE OF INVENTION: Novel full length cDNA			
FILE REFERENCE: 084335-0191			
CURRENT APPLICATION NUMBER: US/11/072,512			
CURRENT FILING DATE: 2005-03-07			
PRIOR APPLICATION NUMBER: US 60/350,978			
PRIOR FILING DATE: 2002-01-25			
PRIOR APPLICATION NUMBER: JP 2001-379298			
PRIOR FILING DATE: 2001-11-05			
NUMBER OF SEQ ID NOS: 4096			
SOFTWARE: PatentIn Ver. 2.1			
SEQ ID NO 2786			
LENGTH: 429			
TYPE: PRT			
ORGANISM: Homo sapiens			
US-11-072-512-2786			
Query Match			
Best Local Similarity 12.0%; Score 455; DB 7; Length 429;			
Best Local Similarity 34.9%; Pred. No. 8, 2e-26;			
Matches 104; Conservative 40; Mismatches 131; Indels 23; Gaps 7			
Qy	421	ENLIDQSPFKLASGSDSTIPQASRLN--NIVNRSMTGSPRSSSSKSHSPLYVMHPPKCTSC	478
Db	129	ERLNKMKMDFQGVYVEELTRGRGSESKYNDPFGNSFTYNSNLISHQRLPYGDRPHKCDQC	188
Qy	479	GSQSDQHAEMC---LHTAGFTFAEEMGETOSEYSDS-----CENGAFCNEDC	525
Db	169	SXSPFARTSDLIQHQRHTEGKEPY--ECNECGKAFSSSHLIQHQRHTEGKEPYECSDDGK	246
Qy	536	RFSESAIKRHTLOHSDKPYKCDRCQASFRYKGNLASHKTVHTEGKPYRCNICGAQFNRP	585
Db	247	TFSQSSALILHRRHTEGKEPYECNECGKTFEWSSTLTHQRHTEGKEPYACNECGKAFSR	306
Qy	586	PANLKTHTRIHSGEKPCEICGTGAFVQVNLHAAVLIHTEGKEPYCEICGTFRPHLQTL	645
Db	307	SSTLTHQRHTEGKEPYECNECGKAFSSSHLIQHQRHTEGKEPYECCGKFTYSSGL	366

OY 646 KSHLRHTGKPYHCCKNLHFRHKSOL-----RLHLRQKI-GAITTKVOYRSATDL 698
DB 367 IOHORHTGHEPYECSECGAFRYSALVHORIHTEGKPLNGIGMSKSLRVTJ-TEL 423

RESULT 12

US-11-072-512-2053

Sequence 2053, Application US/11072512

Publication No. US2006029945A1

GENERAL INFORMATION:

APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHICO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2053
LENGTH: 504
TYPE: PRT
ORGANISM: Homo sapiens

US-11-072-512-2053

Query Match 12.0%; Score 454.5; DB 7; Length 504;

Best Local Similarity 30.0%; Pred. No. 1.1e-25;

Matches 119; Conservative 42; Mismatches 157; Indels 79; Gaps 12;

OY 349 SSKXACTLOASGSPAKSPDTPKACNMKKYFIVLNSINONAKPG-----GPEQ 397
DB 126 SNSNIHKKROTGGKPEKCEGKSC-----CILSOLTHKKTATRVNFKCTCGKAF 178
OY 398 AELRLSPRAYTAPACOPPEWEPENLDIOSPTKLASGEOSTIPOASRLNINIVRSMTG 457
DB 179 NQENLTKKTIHEV-----NPKCEBGCK-----AFNQSJL-- 211
OY 458 PRSSSESHSLYMH--PPKCTSCG-----SQSPOHAMECLHT-AGPTFAEMGE----- 503
DB 212 ----LTGKKKIHTEEKPYKCEDCGKVSFVSLTGH--KIHTGKPPNCECGKGSIF 265
OY 504 -TOSEYDSSCENAFPCNECDGPFSEASLKRHTLOTHSDKPYKCDRCQASFRYKGMIA 562
DB 266 STLTKHAKIHTGKPYKCEGKAFNWSSTLTGKRIITGKPYKCEGKAFNWSSTLT 325
OY 563 SHKTVHTGKPYKCNICGAOFNRPANLKTHTRIHSGKPYKCEGKAFVVAHLRAVL 622
DB 326 RHKIVHTGKPYKCEGKAFNWSSTLTGKRIITGKPYKCEGKAFVFSSTLTGKI 385
OY 623 IHTGKPYKCEGKAFNWSSTLTGKRIITGKPYKCEGKAFVFSSTLTGKI 678
DB 386 IHTGKPYKCEGKAFNWSSTLTGKRIITGKPYKCEGKAFVFSSTLTGKI 445

OY 679 -----OKGATNTK---VOYRSATDLPPELPKAC 706
DB 446 EKYKCEGKAFNWSSTLTGKRIITGKPYKCEGK 482

RESULT 13

US-11-072-512-2449

Sequence 2449, Application US/11072512

Publication No. US20060029945A1

GENERAL INFORMATION:

APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHICO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2449
LENGTH: 636
TYPE: PRT
ORGANISM: Homo sapiens

US-11-072-512-2449

Query Match 12.0%; Score 454; DB 7; Length 636;

Best Local Similarity 34.9%; Pred. No. 1.6e-25;

Matches 95; Conservative 45; Mismatches 104; Indels 28; Gaps 6;

OY 437 DSTIPQASRLNINIVRSMTG-----SPRSSSESHSLYMH--HPKCTSCGSO 481
DB 280 DKAFNQOSQSH--HRHTGKPYKCECDKVSFSSKSTIETHKRIHTEGKPYKCDVTA 337
OY 482 SPQAEWMC-----LHTAGPT-AEEMGETOSEYDSSCEN-----GAFPCNECDGPFSE 530
DB 338 FTWHSQALRRRIHTAKTYKCEGKTFSSHKSLLVCHHNLHGGKSKYKCDVCAFWWS 397
OY 531 ASLKRHTLOTHSDKPYKCDRCQASFRYKGMIAHKTHTGKPYKCNICGAOFNRPANLX 590
DB 398 SOLAKHTRIDGKPYKCEGKTFGONSLLTHKSIHTGKPYKCEGKAFVFSSTLTGKI 457
OY 591 THTRIHSGKPYKCEGKAFVVAHLRAVL IHTGKPYKCEGKAFVVAHLRAVL 650
DB 458 THKIGTGEKPYKCDVCAFWWSSTLTGKRIITGKPYKCEGKAFVFSSTLTGKI 517
OY 651 IHTGKPYKCEGKAFVVAHLRAVL IHTGKPYKCEGKAFVVAHLRAVL 682
DB 518 VHSGEKPYKCEGKAFVVAHLRAVL IHTGKPYKCEGKAFVVAHLRAVL 549

RESULT 14

US-10-517-151-4

Sequence 4, Application US/10517151

Publication No. US20060019252A1

```

: GENERAL INFORMATION:
: APPLICANT: Nakamura, Yusuke
: APPLICANT: Furukawa, Yoichi
: APPLICANT: Oncotherapy Science, Inc.
: APPLICANT: The University of Tokyo
: TITLE OF INVENTION: Genes and Polypeptides Relating to Hepatocellular or
: TITLE OF INVENTION: Colorectal Carcinoma
: FILE REFERENCE: 082379-000400US
: CURRENT APPLICATION NUMBER: US/10/517.151
: CURRENT FILING DATE: 2004-12-06
: PRIOR APPLICATION NUMBER: US 60/386,985
: PRIOR FILING DATE: 2002-06-06
: PRIOR APPLICATION NUMBER: WO PCT/JP03/07070
: PRIOR FILING DATE: 2003-06-04
: NUMBER OF SEQ ID NOS: 111
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 4
: LENGTH: 500
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-10-517-151-4

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 2, 2006, 04:05:02 ; Search time 167 Seconds
(without alignments)
1766.392 Million cell updates/sec

Title: US-10-755-889-18

Perfect score: 3793
Sequence: 1 MASPADSCIOFTRHSDVLL.....TKYQVRVSATDLPPELPKAC 706

Scoring table: BLOSUM62
Gapco 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications_AA_Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3793	100.0	706	4	US-10-755-889-18 Sequence 18, Appl
2	3777	99.6	706	4	US-10-755-889-66 Sequence 66, Appl
3	3771	99.4	706	4	US-10-408-765A-1988 Sequence 1988, Ap
4	3763	99.2	706	3	US-09-107-058-2 Sequence 2, Appl1
5	3763	99.2	706	3	US-09-764-117-2 Sequence 2, Appl1
6	1155	30.5	479	4	US-10-295-027-16 Sequence 16, Appl
7	1155	30.5	479	4	US-10-211-462-24 Sequence 24, Appl
8	1122.5	29.6	518	3	US-09-815-379-4 Sequence 4, Appl1
9	618.5	16.3	810	5	US-10-974-440-27 Sequence 27, Appl
10	610	16.1	803	9	US-10-441-854-9 Sequence 9, Appl1
11	564.5	14.9	765	5	US-10-486-977-12 Sequence 12, Appl
12	560	14.8	110	3	US-09-107-058-9 Sequence 9, Appl1
13	560	14.8	110	3	US-09-764-117-9 Sequence 9, Appl1
14	552	14.6	108	4	US-10-164-359-3 Sequence 3, Appl1
15	540	14.2	688	5	US-10-477-646-21 Sequence 21, Appl
16	522.5	13.8	610	4	US-10-221-625-10 Sequence 10, Appl
17	517	13.6	711	4	US-10-034-934-90 Sequence 90, Appl
18	504	13.3	678	4	US-10-296-115-1316 Sequence 1316, Ap
19	503	13.3	799	4	US-10-104-047-2929 Sequence 2929, Ap
20	501	13.2	673	5	US-10-756-149-4775 Sequence 4775, Ap
21	501	13.2	819	4	US-10-108-260A-3302 Sequence 3302, Ap
22	497.5	13.1	1050	5	US-10-450-763-40044 Sequence 40044, A
23	497	13.1	458	4	US-10-408-765A-2340 Sequence 2340, Ap
24	495.5	13.1	638	5	US-10-723-860-1613 Sequence 1613, Ap
25	494.5	13.0	597	4	US-10-136-728-58 Sequence 58, Appl
26	494	13.0	595	4	US-10-203-052B-8 Sequence 8, Appl
27	492	13.0	1520	5	US-10-450-763-57489 Sequence 57489, A

28	490.5	12.9	606	4	US-10-074-978A-117 Sequence 117, App
29	489	12.9	340	5	US-10-450-763-35320 Sequence 35320, A
30	488.5	12.9	587	4	US-10-029-386-32268 Sequence 32268, A
31	488	12.9	464	4	US-10-108-260A-3590 Sequence 3590, Ap
32	486.5	12.8	577	4	US-10-381-327-3 Sequence 3, Appl1
33	486.5	12.8	613	4	US-10-408-765A-1517 Sequence 1517, Ap
34	485.5	12.8	498	4	US-10-094-749-1657 Sequence 1657, Ap
35	485.5	12.8	517	5	US-10-450-763-33734 Sequence 33734, A
36	485	12.8	832	5	US-10-450-763-40902 Sequence 40902, A
37	483.5	12.7	406	5	US-09-764-864-976 Sequence 976, App
38	483	12.7	458	5	US-10-719-993-448 Sequence 448, App
39	483	12.7	458	5	US-10-719-993-449 Sequence 449, App
40	483	12.7	488	3	US-09-840-787-17 Sequence 17, Appl
41	483	12.7	803	4	US-10-408-765A-1049 Sequence 1049, Ap
42	479	12.6	632	5	US-10-450-763-48745 Sequence 48745, A
43	477	12.6	540	4	US-10-029-386-32905 Sequence 32905, A
44	476.5	12.6	697	4	US-10-408-765A-2256 Sequence 2256, Ap
45	476.5	12.6	697	5	US-10-723-860-4408 Sequence 4408, Ap

ALIGNMENTS

RESULT 1									
US-10-755-889-18									
Sequence 18, Application US/10755889									
Publication No. US20040171823A1									
GENERAL INFORMATION:									
APPLICANT: Bristol-Myers Squibb Company									
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB									
TITLE OR INVENTION: PATHWAY									
FILE REFERENCE: D0284 NP									
CURRENT APPLICATION NUMBER: US/10/755, 889									
CURRENT FILING DATE: 2004-01-13									
PRIOR APPLICATION NUMBER: U.S. 60/440, 068									
PRIOR FILING DATE: 2003-01-14									
PRIOR APPLICATION NUMBER: U.S. 60/469, 757									
PRIOR FILING DATE: 2003-05-12									
NUMBER OF SEQ ID NOS: 823									
SOFTWARE: PatentIn version 3.2									
SEQ ID NO 18									
LENGTH: 706									
TYPE: PRT									
ORGANISM: Homo sapiens									
US-10-755-889-18									
Query Match									
Best Local Similarity 100.0%; Score 3793; DB 4; Length 706;									
Matches 706; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	MAFPADSCIOFTRHSDVLLINLRKSRDILITDVIVYSRBOFPAKTVLMACGGLFYSI	60						
Db	1	MAFPADSCIOFTRHSDVLLINLRKSRDILITDVIVYSRBOFPAKTVLMACGGLFYSI	60						
Qy	61	FTTDLKKNLIVINLDEPINEGFCILLDFMTSLNREGINAVMATYMLQHEHYVDI	120						
Db	61	FTTDLKKNLIVINLDEPINEGFCILLDFMTSLNREGINAVMATYMLQHEHYVDI	120						
Qy	121	CRKTKASAEAMVSAIKPRPEEFNLSHMLPQDIMAAYRGVEVNNILPLRSAPCCESRAF	180						
Db	121	CRKTKASAEAMVSAIKPRPEEFNLSHMLPQDIMAAYRGVEVNNILPLRSAPCCESRAF	180						
Qy	181	APSLYSGLSITPPASYSMTSHLPVSSLLFSDBEFRDVMPPVAPNPPKRRALPCDSARVPKG	240						
Db	181	APSLYSGLSITPPASYSMTSHLPVSSLLFSDBEFRDVMPPVAPNPPKRRALPCDSARVPKG	240						
Qy	241	EYSRPTLEVSPNCHSNIVSPKETTPEARSDDMYVAEGIKPAAPSARNAPYPCCKAS	300						
Db	241	EYSRPTLEVSPNCHSNIVSPKETTPEARSDDMYVAEGIKPAAPSARNAPYPCCKAS	300						
Qy	301	KEERPSSEDEIALHFPFPNAPLNKRGLVSPQSPKSDCOPNSPTEACSSKNACITLQASG	360						
Db	301	KEERPSSEDEIALHFPFPNAPLNKRGLVSPQSPKSDCOPNSPTEACSSKNACITLQASG	360						

QY 361 SPPAKSPDPAKCNMCKKYFIVLNSLNQNAKPGPQAEIGRLSPRAYTAPACOPMMP 420
 DB 361 SPPAKSPDPAKCNMCKKYFIVLNSLNQNAKPGPQAEIGRLSPRAYTAPACOPMMP 420
 QY 421 ENLDIOSPTKLASGSDSTIPOASRLNNTVNSMTGSPRSSSESHPLYMHPKCTSCGS 480
 DB 421 ENLDIOSPTKLASGSDSTIPOASRLNNTVNSMTGSPRSSSESHPLYMHPKCTSCGS 480
 QY 481 OSPQHAEMCLHTAGPTFAEEMGETOSEYSDSCENGAFFCNECDRCFSEBASLKHHTLOT 540
 DB 481 OSPQHAEMCLHTAGPTFAEEMGETOSEYSDSCENGAFFCNECDRCFSEBASLKHHTLOT 540
 QY 541 HSDKPYKCDRCQASFRYKGNLASHKTVHTGKPYPCNICGAQFNRPAULKHTTRJHSGBK 600
 DB 541 HSDKPYKCDRCQASFRYKGNLASHKTVHTGKPYPCNICGAQFNRPAULKHTTRJHSGBK 600
 QY 601 PYKCECGARFQVAHLRAHVLHTGKPYPCNICGAQFNRPAULKHTTRJHSGBK 660
 DB 601 PYKCECGARFQVAHLRAHVLHTGKPYPCNICGAQFNRPAULKHTTRJHSGBK 660
 QY 661 EKCNLHFRHKSQRLRLRQKHGAIINTKYQYRVASATDLPPELPKAC 706
 DB 661 EKCNLHFRHKSQRLRLRQKHGAIINTKYQYRVASATDLPPELPKAC 706

RESULT 2

US-10-755-889-66
 ; Sequence 66, Application US/10755889
 ; Publication No. US20040171823A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
 ; FILE REFERENCE: D0284 NP
 ; CURRENT APPLICATION NUMBER: US/10/755,889
 ; PRIOR FILING DATE: 2004-01-13
 ; PRIOR APPLICATION NUMBER: U.S. 60/440,068
 ; PRIOR FILING DATE: 2003-01-14
 ; PRIOR APPLICATION NUMBER: U.S. 60/469,757
 ; PRIOR FILING DATE: 2003-05-12
 ; NUMBER OF SEQ ID NOS: 823
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 66
 ; LENGTH: 706
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-755-889-66

Query Match 99.6%; Score 3777; DB 4; Length 706;
 Best Local Similarity 99.6%; Pred. No. 7,4e-239;
 Matches 703; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MASPADSCIOFTRHASDVLNLTNRLRSRDILTVDVIIVSRBOPRAHKTVMACSGLFYSI 60
 DB 1 MASPADSCIOFTRHASDVLNLTNRLRSRDILTVDVIIVSRBOPRAHKTVMACSGLFYSI 60
 QY 61 FTDLKCNLSVINLDEINDEGFCILLDFMTYSRLNLRGNIMAVATAMYLQMEHVDT 120
 DB 61 FTDLKCNLSVINLDEINDEGFCILLDFMTYSRLNLRGNIMAVATAMYLQMEHVDT 120
 QY 121 CRKFTIASEAEWVAIKPREEFILNSRMLMPODIMAYRGREVENNLPLRSAPGCSRAAF 180
 DB 121 CRKFTIASEAEWVAIKPREEFILNSRMLMPODIMAYRGREVENNLPLRSAPGCSRAAF 180
 QY 181 APSLYSGLSTPPASYSWYSHLPVSSILFSDDEFRDVMPVAMPFKERALPCDSAPVPVG 240
 DB 181 APSLYSGLSTPPASYSWYSHLPVSSILFSDDEFRDVMPVAMPFKERALPCDSAPVPVG 240
 QY 241 EYSRPTLEVPVNCNSNITSPKKTIPERASDMHYVAABGLKPAAPBARNAFFPCDKAS 300
 DB 241 EYSRPTLEVPVNCNSNITSPKKTIPERASDMHYVAABGLKPAAPBARNAFFPCDKAS 300

QY 301 KEERSSSEDEIALHFEPPNAPLNKGLVSPQSPKSDCCQNSPTACSSKNACILQASG 360
 DB 301 KEERSSSEDEIALHFEPPNAPLNKGLVSPQSPKSDCCQNSPTACSSKNACILQASG 360
 QY 361 SPPAKSPDPAKCNMCKKYFIVLNSLNQNAKPGPQAEIGRLSPRAYTAPACOPMMP 420
 DB 361 SPPAKSPDPAKCNMCKKYFIVLNSLNQNAKPGPQAEIGRLSPRAYTAPACOPMMP 420
 QY 421 ENLDIOSPTKLASGSDSTIPOASRLNNTVNSMTGSPRSSSESHPLYMHPKCTSCGS 480
 DB 421 ENLDIOSPTKLASGSDSTIPOASRLNNTVNSMTGSPRSSSESHPLYMHPKCTSCGS 480
 QY 481 OSPQHAEMCLHTAGPTFAEEMGETOSEYSDSCENGAFFCNECDRCFSEBASLKHHTLOT 540
 DB 481 OSPQHAEMCLHTAGPTFAEEMGETOSEYSDSCENGAFFCNECDRCFSEBASLKHHTLOT 540
 QY 541 HSDKPYKCDRCQASFRYKGNLASHKTVHTGKPYPCNICGAQFNRPAULKHTTRJHSGBK 600
 DB 541 HSDKPYKCDRCQASFRYKGNLASHKTVHTGKPYPCNICGAQFNRPAULKHTTRJHSGBK 600
 QY 601 PYKCECGARFQVAHLRAHVLHTGKPYPCNICGAQFNRPAULKHTTRJHSGBK 660
 DB 601 PYKCECGARFQVAHLRAHVLHTGKPYPCNICGAQFNRPAULKHTTRJHSGBK 660
 QY 661 EKCNLHFRHKSQRLRLRQKHGAIINTKYQYRVASATDLPPELPKAC 706
 DB 661 EKCNLHFRHKSQRLRLRQKHGAIINTKYQYRVASATDLPPELPKAC 706

RESULT 3

US-10-408-765A-1988
 ; Sequence 1988, Application US/10408765A
 ; Publication No. US20040101874A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ghosh, Soumitra S.
 ; APPLICANT: Fahy, Boia D.
 ; APPLICANT: Zhang, Bing
 ; APPLICANT: Gibson, Bradford W.
 ; APPLICANT: Taylor, Steven W.
 ; APPLICANT: Glenn, Gary M.
 ; APPLICANT: Warnock, Dale E.
 ; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
 ; FILE REFERENCE: 660088,465
 ; CURRENT APPLICATION NUMBER: US/10/408,765A
 ; CURRENT FILING DATE: 2003-04-04
 ; NUMBER OF SEQ ID NOS: 3077
 ; SOFTWARE: FaastSeq for Windows Version 4.0
 ; SEQ ID NO 1988
 ; LENGTH: 706
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-408-765A-1988

Query Match 99.4%; Score 3771; DB 4; Length 706;
 Best Local Similarity 99.4%; Pred. No. 1.8e-238;
 Matches 702; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MASPADSCIOFTRHASDVLNLTNRLRSRDILTVDVIIVSRBOPRAHKTVMACSGLFYSI 60
 DB 1 MASPADSCIOFTRHASDVLNLTNRLRSRDILTVDVIIVSRBOPRAHKTVMACSGLFYSI 60
 QY 61 FTDLKCNLSVINLDEINDEGFCILLDFMTYSRLNLRGNIMAVATAMYLQMEHVDT 120
 DB 61 FTDLKCNLSVINLDEINDEGFCILLDFMTYSRLNLRGNIMAVATAMYLQMEHVDT 120
 QY 121 CRKFTIASEAEWVAIKPREEFILNSRMLMPODIMAYRGREVENNLPLRSAPGCSRAAF 180
 DB 121 CRKFTIASEAEWVAIKPREEFILNSRMLMPODIMAYRGREVENNLPLRSAPGCSRAAF 180
 QY 181 APSLYSGLSTPPASYSWYSHLPVSSILFSDDEFRDVMPVAMPFKERALPCDSAPVPVG 240
 DB 181 APSLYSGLSTPPASYSWYSHLPVSSILFSDDEFRDVMPVAMPFKERALPCDSAPVPVG 240

QY 241 EYSRPTLEVPNVCHSNISYPKETIPEARS DMHYSVAEGLKPAASARNAFYPPCDKAS 300
 DB 241 EYSRPTLEVPNVCHSNISYPKETIPEARS DMHYSVAEGLKPAASARNAFYPPCDKAS 300
 QY 301 KEERPESSDEIALHFEPPNAPLNKGLVSPQSPKSDCCPNSTPTEACSSKNACILQASG 360
 DB 301 KEERPESSDEIALHFEPPNAPLNKGLVSPQSPKSDCCPNSTPTEACSSKNACILQASG 360
 QY 361 SPPAKSPTDPKACMCKYKFI VINSLNQNAKPGPEQAEIGRLSPRAYTAPPAQCPMPER 420
 DB 361 SPPAKSPTDPKACMCKYKFI VINSLNQNAKPGPEQAEIGRLSPRAYTAPPAQCPMPER 420
 QY 421 ENLDOSPTKLSASGEDSTIPOASRLNNIVNRSMTGSPRSSSHSPLVHMPKCTSCGS 480
 DB 421 ENLDOSPTKLSASGEDSTIPOASRLNNIVNRSMTGSPRSSSHSPLVHMPKCTSCGS 480
 QY 481 QSPQHAMCMTHTAGPTFAEMGETQSEYSDSSCENGAFCNECDRCRSEASLKRHTLOT 540
 DB 481 QSPQHAMCMTHTAGPTFAEMGETQSEYSDSSCENGAFCNECDRCRSEASLKRHTLOT 540
 QY 541 HSDKPYKCDRCQASFRYKGNLASHKVTHTGKPYRCNICGAQFNR PANLKTHTRIHSGEK 600
 DB 541 HSDKPYKCDRCQASFRYKGNLASHKVTHTGKPYRCNICGAQFNR PANLKTHTRIHSGEK 600
 QY 601 PYKCTCGARFVQVAHLRAVHLIHTGKPYPCICGTRFRHLQTLKSHLR IHTGEKPYHC 660
 DB 601 PYKCTCGARFVQVAHLRAVHLIHTGKPYPCICGTRFRHLQTLKSHLR IHTGEKPYHC 660
 QY 661 EKNLHFRHKSQLRHLRQKHGAITNTKQYRVASATDLPPELPRAC 706
 DB 661 EKNLHFRHKSQLRHLRQKHGAITNTKQYRVASATDLPPELPRAC 706

RESULT 4
 US-09-107-058-2
 ; Sequence 2, Application US/09107058
 ; Patent No. US20010010922A1
 GENERAL INFORMATION:
 APPLICANT: Dalla-Favera, Riccardo
 APPLICANT: Niu, Hui-Peng
 TITLE OF INVENTION: CLONING AND USES OF THE GENETIC
 TITLE OF INVENTION: LOCUS bcl-6
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Cooper & Dunham LLP
 STREET: 1185 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/107,058
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 0575/43771-A-PCT-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 278-0400
 TELEFAX: (212) 391-0525
 TELEX: 422523 COOP UT
 INFORMATION FOR SEO ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 706 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-107-058-2

Query Match 99.3%; Score 3763; DB 3; Length 706;
 Best Local Similarity 99.3%; Pred. No. 6,1e-238;
 Matches 701; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MASPASCTQFTHADVLNLRSLRDLTVIVSVSEOPRAKTVLMACSGFYSI 60
 DB 1 MASPASCTQFTHADVLNLRSLRDLTVIVSVSEOPRAKTVLMACSGFYSI 60
 QY 61 FTDLKCNLSVINLDEINDEGFCILDFMYTSRLNLRBNINAVATAMVTLQMEHVDT 120
 DB 61 FTDLKCNLSVINLDEINDEGFCILDFMYTSRLNLRBNINAVATAMVTLQMEHVDT 120
 QY 121 CRKFIRASEAEWVAIKPPEEFINSRMIMPQDIAYRGREVENNLPLRSAGCESRAF 180
 DB 121 CRKFIRASEAEWVAIKPPEEFINSRMIMPQDIAYRGREVENNLPLRSAGCESRAF 180
 QY 181 APSLYSGLSTPPASYSMTSLPVSSLLFSDSEFRDVMVPANPEPKERALPCDSARVPG 240
 DB 181 APSLYSGLSTPPASYSMTSLPVSSLLFSDSEFRDVMVPANPEPKERALPCDSARVPG 240
 QY 241 EYSRPTLEVPNVCHSNISYPKETIPEARS DMHYSVAEGLKPAASARNAFYPPCDKAS 300
 DB 241 EYSRPTLEVPNVCHSNISYPKETIPEARS DMHYSVAEGLKPAASARNAFYPPCDKAS 300
 QY 301 KEERPESSDEIALHFEPPNAPLNKGLVSPQSPKSDCCPNSTPTEACSSKNACILQASG 360
 DB 301 KEERPESSDEIALHFEPPNAPLNKGLVSPQSPKSDCCPNSTPTEACSSKNACILQASG 360
 QY 361 SPPAKSPTDPKACMCKYKFI VINSLNQNAKPGPEQAEIGRLSPRAYTAPPAQCPMPER 420
 DB 361 SPPAKSPTDPKACMCKYKFI VINSLNQNAKPGPEQAEIGRLSPRAYTAPPAQCPMPER 420
 QY 421 ENLDOSPTKLSASGEDSTIPOASRLNNIVNRSMTGSPRSSSHSPLVHMPKCTSCGS 480
 DB 421 ENLDOSPTKLSASGEDSTIPOASRLNNIVNRSMTGSPRSSSHSPLVHMPKCTSCGS 480
 QY 481 QSPQHAMCMTHTAGPTFAEMGETQSEYSDSSCENGAFCNECDRCRSEASLKRHTLOT 540
 DB 481 QSPQHAMCMTHTAGPTFAEMGETQSEYSDSSCENGAFCNECDRCRSEASLKRHTLOT 540
 QY 541 HSDKPYKCDRCQASFRYKGNLASHKVTHTGKPYRCNICGAQFNR PANLKTHTRIHSGEK 600
 DB 541 HSDKPYKCDRCQASFRYKGNLASHKVTHTGKPYRCNICGAQFNR PANLKTHTRIHSGEK 600
 QY 601 PYKCTCGARFVQVAHLRAVHLIHTGKPYPCICGTRFRHLQTLKSHLR IHTGEKPYHC 660
 DB 601 PYKCTCGARFVQVAHLRAVHLIHTGKPYPCICGTRFRHLQTLKSHLR IHTGEKPYHC 660
 QY 661 EKNLHFRHKSQLRHLRQKHGAITNTKQYRVASATDLPPELPRAC 706
 DB 661 EKNLHFRHKSQLRHLRQKHGAITNTKQYRVASATDLPPELPRAC 706

RESULT 5
 US-09-761-117-2
 ; Sequence 2, Application US/09761117
 ; Patent No. US20010012887A1
 GENERAL INFORMATION:
 APPLICANT: Dalla-Favera, Riccardo
 APPLICANT: Chaganti, Raju S.K.
 TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS
 TITLE OF INVENTION: bcl-6
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Cooper & Dunham LLP
 STREET: 1185 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10036

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/761,117
FILING DATE: 16-Jan-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/43771-A-PCT-US-Y
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 706 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-761-117-2

Query Match      99.2%; Score 3763; DB 3; Length 706;
Best Local Similarity 99.3%; Pred. No. 6.1e-238;
Matches 701; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

1 MASPADSCIOFTTHASDVLTNLRSLRDILDTVVIVSRQOPRAKVTLMACSGFYSTI 60
1 MASPADSCIOFTTHASDVLTNLRSLRDILDTVVIVSRQOPRAKVTLMACSGFYSTI 60
61 FTDLKCNLSVINLDEINDEGFCILDFWYTSRLNLRGNINAVATAMTYLQMEHVDT 120
61 FTDLKCNLSVINLDEINDEGFCILDFWYTSRLNLRGNINAVATAMTYLQMEHVDT 120
121 CRKFTKASEAMVSAIKPRPEEFNLNRMMPQIMAYRGREVENNLPLRSAGCCSRAP 180
121 CRKFTKASEAMVSAIKPRPEEFNLNRMMPQIMAYRGREVENNLPLRSAGCCSRAP 180
181 APSLISGLSTPPASYSNYSHLPVSSLLFSDDEFRDVMYANPFPKERALPCDSAPVRG 240
181 APSLISGLSTPPASYSNYSHLPVSSLLFSDDEFRDVMYANPFPKERALPCDSAPVRG 240
241 EYSRPTLEVPNYCHSNIVSPKKTIEBEASDMHYVAEGLKPAASARNAPYPCDKAS 300
241 EYSRPTLEVPNYCHSNIVSPKKTIEBEASDMHYVAEGLKPAASARNAPYPCDKAS 300
301 KEERPSSEDEIALHFEPPNAPLNKGLVSPQSPKSDCQPNPTEACSSKNACTIQASG 360
301 KEERPSSEDEIALHFEPPNAPLNKGLVSPQSPKSDCQPNPTEACSSKNACTIQASG 360
361 SPPAKSPTDKACSMKKYKFTIVNSLQNAKPGGPEOAEIGRLSPRAYTAPPCOPMPE 420
361 SPPAKSPTDKACSMKKYKFTIVNSLQNAKPGGPEOAEIGRLSPRAYTAPPCOPMPE 420
421 ENLDLQSPYTLASAGSDSTIPOSRLNNIVNRSMTGSPRSSSESHSPLVYHMPKCTSCG 480
421 ENLDLQSPYTLASAGSDSTIPOSRLNNIVNRSMTGSPRSSSESHSPLVYHMPKCTSCG 480
481 QSPQHAEMCLHTAGPTFAEMGETQSFSPSSCENGAFPCNEDCRFSEASLKRHTLOT 540
481 QSPQHAEMCLHTAGPTFAEMGETQSFSPSSCENGAFPCNEDCRFSEASLKRHTLOT 540
541 HSDKPYKCDRCQASFRKGNLASHKIVHTSEKPRNCICGAQFRPNNLTKTHRIHSGEK 600
541 HSDKPYKCDRCQASFRKGNLASHKIVHTSEKPRNCICGAQFRPNNLTKTHRIHSGEK 600
601 PYKCTGCAFRVQVLAHRAVLLHTGKRPYPCICGTFRHLQTLKSHLRHTGKRPYHC 660
601 PYKCTGCAFRVQVLAHRAVLLHTGKRPYPCICGTFRHLQTLKSHLRHTGKRPYHC 660

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661 EKNLHFRKSQLRLHLRQKHGATNTKYQYVSATDLPPELPKAC 706
661 EKNLHFRKSQLRLHLRQKHGATNTKYQYVSATDLPPELPKAC 706

RESULT 6
US-10-295-027-16
Sequence 16, Application US/10295027
Publication No. US2003023250A1
GENERAL INFORMATION:
APPLICANT: Afari, Daniel
APPLICANT: Aziz, Natacha
APPLICANT: Gineberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Glynn, Richard
APPLICANT: Hevezl, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
FILE REFERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
PRIOR FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 09/663,733
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/347,393
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR FILING DATE: 2002-02-13
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 1386
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16
LENGTH: 479
TYPE: PRT
ORGANISM: Homo sapiens
US-10-295-027-16

Query Match      30.5%; Score 1155; DB 4; Length 479;
Best Local Similarity 38.3%; Pred. No. 2.6e-67;
Matches 268; Conservative 58; Mismatches 142; Indels 232; Gaps 15;

1 MASPA--DSCI-----QFTTHASDVLTNLRSLRDILDTVVIVSRQOPRAKVTLMACSG 54
1 MASPA--DSCI-----QFTTHASDVLTNLRSLRDILDTVVIVSRQOPRAKVTLMACSG 54
1 MGSAPABGALGVNFEHTSSDVLGNLNLRLRGILDTVTLLVGGQPLRAKAVLIACS 60
1 MGSAPABGALGVNFEHTSSDVLGNLNLRLRGILDTVTLLVGGQPLRAKAVLIACS 60
55 GLPYSTFTDLKCNLSVINLDEINDEGFCILDFWYTSRLNLRGNINAVATAMTYLQ 114
55 GLPYSTFTDLKCNLSVINLDEINDEGFCILDFWYTSRLNLRGNINAVATAMTYLQ 114
61 GFYSIFRRAGAGVDVLSLPGPEARGFAPLDFWYTSRLNLSPTATDAVVAATAATYLO 120
61 GFYSIFRRAGAGVDVLSLPGPEARGFAPLDFWYTSRLNLSPTATDAVVAATAATYLO 120
115 EHVVDTCRKFTKASEAMVSAIKPRPEEFNLNRMMPQIMAYRGREVENNLPLRSAGD 174
115 EHVVDTCRKFTKASEAMVSAIKPRPEEFNLNRMMPQIMAYRGREVENNLPLRSAGD 174
121 EHVVDTCRKFTKASEAMVSAIKPRPEEFNLNRMMPQIMAYRGREVENNLPLRSAGD 174
121 EHVVDTCRKFTKASEAMVSAIKPRPEEFNLNRMMPQIMAYRGREVENNLPLRSAGD 174
175 CESRAPAPSLVSGLSTPPASYSNYSHLPVSSLLFSDDEFRDVMYANPFPKERALPCDS 234
175 CESRAPAPSLVSGLSTPPASYSNYSHLPVSSLLFSDDEFRDVMYANPFPKERALPCDS 234

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Db 135 -----YEPGIS----- 141
 QY 235 ARPVGYSRPTLEVPNVCHSNISPKETIPERASDMHYSVAEGLKPAASARNAPYF 294
 Db 142 -----LRPL----- 145
 QY 295 PCDKASKEBERPSEDEIALHFEPPNAPLNKGLVSPQSPKSDCCPNPTEACSSKNAC 354
 Db 146 -----EABPPT-----PPTAP-----PGSPRRSGHDPPTESRS----- 176
 QY 355 ILQASGSPPAKSPDPACNWKYKFTVLSNINAKGPGBOAELGRLSPRAYTAPAC 414
 Db 177 ---CSGPPSPASDPDPACNWKYKFTVLSNINAKGPGBOAELGRLSPRAYTAPAC 223
 QY 415 QPMEPENLDQSPTKLSASGEDSTIP-QASRLNINVRSMWTSPPRSSSESHSPLVHMP 473
 Db 224 QARLPSEDEASSSSSSSEBGPDPGOSRL-----SPTATVOF----- 265
 QY 474 KCTSGSGSPQHAEMCHTAGPTPAEEMGETQSEYSDSCENGAFPCNECCRSSEASL 533
 Db 266 ---KCG--APASTPYLLTSQ---AODTSGSPSRARPLPGSEFFSCONCEAVAGCSSGL 316
 QY 534 KRHTLQTHSDKPYKCDRCQASFRYKGNLASHKVTHTGKPYRCNICGAQFNRPANLKTHT 593
 Db 317 D-SLVPGDEDEKPYKQLCRSFRYKGNLASHKVTHTGKPYRCNICGAQFNRPANLKTHT 375
 QY 594 RHSGEKPYKCTCGARFVOVAHLRAVLIHTGKPYRCNICGAQFNRPANLKTHT 653
 Db 376 RHSGEKPYKCTCGARFVOVAHLRAVLIHTGKPYRCNICGAQFNRPANLKTHT 435
 QY 654 GEKPYHCEKNLHFRHKSQRLHLRQKHGAATNTKVHYI 693
 Db 436 GEKPYHCEKNLHFRHKSQRLHLRQKHGAATNTKVHYI 475

RESULT 7

US-10-211-462-24
 ; Sequence 24, Application US/10211462
 ; Publication No. US2004003495A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Murray, Richard
 ; APPLICANT: Glynn, Richard
 ; APPLICANT: Watson, Susan R.
 ; APPLICANT: Aziz, Natasha
 ; APPLICANT: Eos Biotechnology, Inc.
 ; TITLE OF INVENTION: Methods of diagnosis of Angiogenesis. Compositions and
 ; FILE REFERENCE: 018501-006200US
 ; CURRENT FILING DATE: US/10/211,462
 ; PRIOR FILING DATE: 2003-02-13
 ; PRIOR APPLICATION NUMBER: US 09/784,356
 ; PRIOR FILING DATE: 2001-02-14
 ; PRIOR APPLICATION NUMBER: US 09/791,390
 ; PRIOR FILING DATE: 2001-02-22
 ; PRIOR APPLICATION NUMBER: US 60/310,025
 ; PRIOR FILING DATE: 2001-08-03
 ; PRIOR APPLICATION NUMBER: US 60/334,244
 ; PRIOR FILING DATE: 2001-11-29
 ; NUMBER OF SEQ ID NOS: 230
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 24
 ; LENGTH: 479
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-211-462-24

Query Match 30.5%; Score 1155; DB 4; Length 479;
 Best Local Similarity 38.3%; Pred. No. 2,6e-67;
 Matches 268; Conservative 58; Mismatches 142; Indels 232; Gaps 15;
 QY 1 MASPA--DSCI-----QFTHASDVLTNLRSLDILTDVIVVSREQFRHAKVTLMACS 54
 Db 1 MASPAPEGALGVYVEFTTHSSSDVIGNLRLRGLITDVTLLVGGQPLRAHKAVALIACS 60

QY 55 GLEYSITFDQKCNLSVINLDEPEINDEGFCILLDFWYTSRLNIREGINAMVATAMYLQ 114
 Db 61 GFYSISIFRGAGVGVVDLSLPGCEBARGFAPLDFMTTSLRLSPATAPVLAATYLOM 120
 QY 115 EHVDTCKRKFKAEEAMVSAIKPREEFLNSMLMPODIWAYGREVENNLPLRSAPG 174
 Db 121 EHVQACHRIQNS----- 134
 QY 175 CESRAFAPSLSGLSTPPASISWYSHLPVSSLFSDSEFVDVMPVANPPFKERALPCDS 234
 Db 135 -----YEPGIS----- 141
 QY 235 ARPVGYSRPTLEVPNVCHSNISPKETIPERASDMHYSVAEGLKPAASARNAPYF 294
 Db 142 -----LRPL----- 145
 QY 295 PCDKASKEBERPSEDEIALHFEPPNAPLNKGLVSPQSPKSDCCPNPTEACSSKNAC 354
 Db 146 -----EABPPT-----PPTAP-----PGSPRRSGHDPPTESRS----- 176
 QY 355 ILQASGSPPAKSPDPACNWKYKFTVLSNINAKGPGBOAELGRLSPRAYTAPAC 414
 Db 177 ---CSGPPSPASDPDPACNWKYKFTVLSNINAKGPGBOAELGRLSPRAYTAPAC 223
 QY 415 QPMEPENLDQSPTKLSASGEDSTIP-QASRLNINVRSMWTSPPRSSSESHSPLVHMP 473
 Db 224 QARLPSEDEASSSSSSSEBGPDPGOSRL-----SPTATVOF----- 265
 QY 474 KCTSGSGSPQHAEMCHTAGPTPAEEMGETQSEYSDSCENGAFPCNECCRSSEASL 533
 Db 266 ---KCG--APASTPYLLTSQ---AODTSGSPSRARPLPGSEFFSCONCEAVAGCSSGL 316
 QY 534 KRHTLQTHSDKPYKCDRCQASFRYKGNLASHKVTHTGKPYRCNICGAQFNRPANLKTHT 593
 Db 317 D-SLVPGDEDEKPYKQLCRSFRYKGNLASHKVTHTGKPYRCNICGAQFNRPANLKTHT 375
 QY 594 RHSGEKPYKCTCGARFVOVAHLRAVLIHTGKPYRCNICGAQFNRPANLKTHT 653
 Db 376 RHSGEKPYKCTCGARFVOVAHLRAVLIHTGKPYRCNICGAQFNRPANLKTHT 435
 QY 654 GEKPYHCEKNLHFRHKSQRLHLRQKHGAATNTKVHYI 693
 Db 436 GEKPYHCEKNLHFRHKSQRLHLRQKHGAATNTKVHYI 475

RESULT 8

US-09-815-379-4
 ; Sequence 4, Application US/09815379
 ; Publication No. US20030073613A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RASTELI, LUCA
 ; APPLICANT: GERITSEN, MARY
 ; TITLE OF INVENTION: ANGIOGENESIS ASSOCIATED PROTEINS AND NUCLEIC ACIDS
 ; FILE REFERENCE: 10716/35
 ; CURRENT FILING DATE: US/09/815,379
 ; PRIOR FILING DATE: 2001-03-22
 ; PRIOR APPLICATION NUMBER: 60/191,134
 ; PRIOR FILING DATE: 2000-03-22
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 518
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-815-379-4

Query Match 29.6%; Score 1122.5; DB 3; Length 518;
 Best Local Similarity 36.3%; Pred. No. 3.8e-65;
 Matches 268; Conservative 58; Mismatches 142; Indels 271; Gaps 17;
 QY 1 MASPA--DSCI-----QFTHASDVLTNLRSLDILTDVIVVSREQFRHAKVTLMACS 54

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Db      1  MGSPPAREGALGVREFTHSSVDLGNLMBELRGLITVTLLVGGQPLRAKAVLIACS 60
Qy      55  GLEYSITFDOLKCNLSVINLDPREINDEGFCILLDFMYTSRLNREGNINAVATAMYLQ 114
Db      61  GFYYSIFRGRAGVGVVLSLPGPBARGFAPLLDFMYTSRLNLPATAVAALAAATYLOM 120
Qy      115  EHVVDCTKRFIKASLEAMVSATPPREEFPLNSMLMPQIMAVRGEEVENNLPISARG 174
Db      121  EHVVAQCHRTQAS----- 134
Qy      175  CESRAPAPSLYSGLSTPPASYSWYSHLPVSSLLFSDEFRDVMVPVNPFPKERALPCDS 234
Db      135  -----YEPGLIS----- 141
Qy      235  ARDPGEYSRPTLEVPNVCHSNISYPKETTIPPEARSDMHYSVABGLKPAAPARNAPYF 294
Db      142  -----LRPL----- 145
Qy      295  PCDKASKEBERSPSEBDEIALHFFPPNAPLNKGLVSPQSPQSDCCPNSTPTEACSSKNAC 354
Db      146  -----EAPPT-----PPTAP-----PGSPRRSEGHDPPTESRS----- 176
Qy      355  ILQASGSPPAKSPPTDPKACMKKCYKFTVLNLSLNQNAKPGGPBOAELGRLSPRAYTAPAC 414
Db      177  ---CSGPPSPAPDPDKACMKKTKYIVANS-----QASQAGSLVGERSSGQPCP 223
Qy      415  QPPM-BPENLDLQSPTKLASGEDSTIP-QASRLNINIVRSMTSPRSSSESHSPLYMHP 472
Db      224  QALPBGDEASSSSSSSSSSSESGPIPGPSRL-----SPYATVGP----- 266
Qy      473  PKCTSGCSQSPQAEMLHTAGFTFAEMKETSEYSDSCENGAFCECCDRCRBEAS 532
Db      267  ----KCG--APASTPYLLTSQ-----AQDTSGSPSEBARPLPGSEFFSCONCEAVACSSG 316
Qy      533  LKXHTLOTSDKPYKCDRCQASFRYKGNLASHKTYTGKPYKNCIGAOFNPNAMLYKT 592
Db      317  LD-SLVPGDEDKPYKQOLCSSFRYKGNLASHHTVHTGKPYKCSICGARFNRPAIDKH 375
Qy      593  TRIHSGEKPYKCEITCGARFY-----QY 614
Db      376  SRHSGEKPYKCEITCGSRFYQVRSPPSGFGKPARGVGQKGFSSQKDLKSPSPGY 435
Qy      615  AHRRAHYLITGKPYKCEITCGTRFRYLQTLKSHLRHTGKPYKCEKCNLHRAKSOAR 674
Db      436  AHRRAHYLITGKPYKCEITCGTRFRYLQTLKSHLRHTGKPYKCEKCNLHRAKSOAR 495
Qy      675  LHLRQKHGALTNNTKVOYRV 693
Db      496  LHLRQKHGALTNNTKVMYHI 514

RESULT 9
US-10-974-440-27
; Sequence 27, Application US/10974440
; Publication No. US20050214795A1
; GENERAL INFORMATION:
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: BANDMAN, Olga
; APPLICANT: LAL, Preeti
; APPLICANT: YUE, Henry
; APPLICANT: REDDY, Roopa
; APPLICANT: TANG, Y. Tom
; APPLICANT: GERSTIN, Edward H.
; APPLICANT: ARVIZU, Chandra
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: LU, Dying Alina M.
; TITLE OF INVENTION: Human Transcriptional Regulator Molecules
; FILE REFERENCE: PE-0509 USN
; CURRENT APPLICATION NUMBER: US/10/974,440
; CURRENT FILING DATE: 2004-10-26
; PRIOR APPLICATION NUMBER: US/09/674,743

```

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; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/09935
; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 60/084,254
; PRIOR FILING DATE: 1998-05-04
; PRIOR APPLICATION NUMBER: 60/095,827
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/102,745
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PERL Program
; SEQ ID NO 27
; LENGTH: 810
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 1484257CD1
US-10-974-440-27

Query Match      16.3%; Score 618.5; DB 5; Length 810;
Best Local Similarity 26.7%; Pred. No. 6,8e-32;
Matches 200; Conservative 102; Mismatches 298; Indels 149; Gaps 24;

Qy      9  IOFTASADVLNLRNLSRDILTVDVIVSREOPRAHKTVMACSGLYSITFDOLKCN 68
Db      1  MDPFGHSHVLEQLAQKQLGILCDCTFYVDGVHFAKHAVALAACSEYKMLFVQD---- 56
Qy      69  LSVINLDPREINDEGFCILLDFMYTSRLNREGNINAVATAMYLQMEHVVDCTKRFIKAS 128
Db      57  KOVHLHDS-NAAGLGQVLEFMYTAKLSLSPENVVDVLAVALFTLQMODITTACH----- 109
Qy      129  EAMVSATPPREEFPLNSMLMPQIMAVRGEEVENNLPISAPCCSERA----FAPSL 184
Db      110  -----ALKSLAE-----PATSPGNABALAQKCPVPS-PEGDGRAABEKVAYST 153
Qy      185  VS-----GLSTP--PASYSWYSHLPVSSLLFSDEFRDVMVPVNPFPKERALPCDSARP 237
Db      154  LSRLEAGKSTPIGHS-----RDJK-----BERGQAGSAAS 185
Qy      238  VPEYSRPTLEVPNVCHSNISYPKETTIPPEARSDMHYSVABGLKPAAPARNAPYFPCD 297
Db      186  GAEQTEKAD-----APREPPVELKPDPTSGMAALEAALAEALSSBSBDEMEVE 232
Qy      298  KASKEBERSSDEIALHFFPPNAPLNKGL--LVSPQSPQSDCCPNSTPTEACSSKNACI 355
Db      233  PARKSEBQKEBEBEERGAGP-AEVKEKSGOLENGEAEEENESAGTDSGQELG-- 289
Qy      356  LQASG--SPPAKSPPTDPKA-----CNMKKTYFTVANSLNQNAKPGGPBOAELGRLSPR 406
Db      290  -EARGLRSGTYGDRITSKAYGSVIHKCEDCGKFTHTGAFKXHIRHTGKPYKCEKSG 348
Qy      407  AYTAPACQPMPEPENLDLQSPTKLASGEDSTIPQASRLNINIVRSMTSPRSSSESHS 466
Db      349  AFSDPAAACE-----ANEKTHSLPKPYGCEKSGSYRLISLNLHKRHSGBEARVRCEDG 403
Qy      467  PLY-----MH-----PKCTSGCSQSPQAEMLCHHTAGFTFAEMKETSEYSDS 511
Db      404  KLFTHSGNLKRHLQVLHSGKPYQDCYCGRSFDPSTSKMHL-----FTHDTHDKHKCP 456
Qy      512  SCE-----NGAFPCNCCDRCFSEBASIKHTTLOTSHS-DKPYKCDRCQ 552
Db      457  HCDKKNQVGNLKAHLKIHADGRLKRCRCGKQFTTSGNLKHL-LRTHSGEKYVYVLIHQ 515
Qy      553  ASFRYKGNLASHKTYTGKPYKNCIGAOFNPNAPLNKTHTRTHSGEKPYKCEITCGARFY 612
Db      516  RQPADPGALQRYHRIHTGKPYKQCVWCGKAFQASSLAHVNOHTGKPYKCEKRCRFPV 575
Qy      613  QVAHLRAHYLITGKPYKCEITCGTRFRYLQTLKSHLRHTGKPYKCEKCNLHRAKSO 672
Db      576  QSSQLNHTIRHNDHNIHPKCSVCSKAFVWVGDSLKHIIHTGKPYLCKDCGGRFVRVDN 635
Qy      673  LRLHLRQKHGALTNNTKVOYRVSATDLPPE 701

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Db 636 LRSVKTIVHQQKAGIKI-----LEPE 656

RESULT 10
US-10-441-854-9

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1  Sequence 9, Application No.US200400019441854
2  Publication No. US20040028607A1
3  GENERAL INFORMATION:
4  APPLICANT: Brian J. No. US20040028607A1ch
5  APPLICANT: Eric M. Verdin
6  TITLE OF INVENTION: Methods of Modulating
7  TITLE OF INVENTION: Deacetylase Activity
8  FILE REFERENCE: UCL-274
9  CURRENT APPLICATION NUMBER: US/10/441,854
10 CURRENT FILING DATE: 2003-05-19
11 NUMBER OF SEQ ID NOS: 9
12 SOFTWARE: FastSeq for Windows Version 4.0
13 SEQ ID NO 9
14 LENGTH: 803
15 TYPE: prt
16 ORGANISM: H. sapiens
17
18 US-10-441-854-9

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Query Match	16.1%;	Score 610;	DB 4;	Length 803;
Best Local Similarity	26.3%;	Pred. No. 2.4e-31;		
Matches 197;	Conservative 100;	Mismatches 296;	Indels 156;	Gaps 23;

[illegible]

Db 569 QSSQLANHIRHDNIRPHKCSVCRAFNVEDLSKHIIITGEXPYLCDCKGSGFNVDN 628
QY 673 LRHLRQKGALTTNTKQVRVSATDLPPE 701
Db 629 LRSHVKTVAHQGRAGIKI-----LEBP 649

RESULT 11
US-10-486-977-12
; Sequence 12, Application US/10486977
; Publication No. US20050123912A1
; GENERAL INFORMATION:

APPLICANT: INCYTE CORPORATION; BAROSSO, Inese;
APPLICANT: BAUGHN, Mariah R.; BECHA, Shanya D.;
APPLICANT: BLAKE, Julie J.; BOROMSKY, Mark L.;
APPLICANT: BURFORD, Neil; DUGAN, Brendan M.;
APPLICANT: ELLIOTT, Vicki S.; EMBELING, Brooke M.;
APPLICANT: FORSYTHE, Ian F.; GIERZEN, Kimberly J.;
APPLICANT: GORVAD, Ann E.; GRIFFEN, Jennifer A.;
APPLICANT: HANFALTA, April J.A.; HONCHELI, Cynthia D.;
APPLICANT: ISON, Craig H.; KHAN, Farrach A.;
APPLICANT: ILLI, Preci G.; LEE, Ernestine A.;
APPLICANT: LEE, Sally; LEE, Soo Yeun;
APPLICANT: LI, Joana X.; LU, Dyung Anna M.;
APPLICANT: LU, Yan; LEHR-MASON, Patricia M.;
APPLICANT: NGUYEN, Daniel B.; RAMKUTIA, Jayalaxmi;
APPLICANT: SPAGGEO, William W.; TANG, Y. Tom;
APPLICANT: THANGAVELU, Kavitha; THORNTON, Michael B.;
APPLICANT: TRAN, Uylen K.; CHAMLA, Yuminder K.;
APPLICANT: WARREN, Bridget A.; XU, Yuming;
APPLICANT: YAO, Monique G.; YOE, Henry;
APPLICANT: YUE, HuiBin; ZEHARADIAN, Yeganeh
TITLE OF INVENTION: NUCLEIC-ACID ASSOCIATED PROTEINS

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1 FILE REFERENCE: PF-1146 USN
2 CURRENT APPLICATION NUMBER: US/10/486, 977
3 CURRENT FILING DATE: 2004-02-17
4 PRIOR APPLICATION NUMBER: PCT/US02/25829
5 PRIOR FILING DATE: 2002-08-14
6 PRIOR APPLICATION NUMBER: US 60/313, 111
7 PRIOR FILING DATE: 2001-08-17
8 PRIOR APPLICATION NUMBER: US 60/314, 682
9 PRIOR FILING DATE: 2001-08-24
10 PRIOR APPLICATION NUMBER: US 60/314, 756
11 PRIOR FILING DATE: 2001-08-24
12 PRIOR APPLICATION NUMBER: US 60/315, 105
13 PRIOR FILING DATE: 2001-08-27
14 PRIOR APPLICATION NUMBER: US 60/316, 751
15 PRIOR FILING DATE: 2001-08-31
16 PRIOR APPLICATION NUMBER: US 60/316, 856
17 PRIOR FILING DATE: 2001-08-31
18 PRIOR APPLICATION NUMBER: US 60/328, 185
19 PRIOR FILING DATE: 2001-10-05
20 NUMBER OF SEQ ID NOS: 66
21 SOFTWARE: PERL Program
22 SEQ ID NO 12

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? LENGTH: 765
? TYPE: PRF
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: misc_feature
? OTHER INFORMATION: Incyte ID No: 3217430CD1
US-10-486-977-12

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Query Match	14.9%	Score 564.5	DB 5	Length 765	
Best Local Similarity	26.5%	Pred. No. 2.2e+28			
Matches 187	Conservative 30	Mismatches 245		Indels 183	Gaps 22

Qy 14 HASDYLINLNRLSHSDIILTVIVVSRBOFRAHKTVIMACSGLFYSITFDOLKNLSVIN 73
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 7 HSCILLQOIHBEORIGLLCDCKLVKGVCFRKHNVLAASFYFFSLTQNSSSQNDVPH 66
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 74 LDPEINPBGFCILDDFMYSRLNLRGNIMAVMATAMYLQMEHVVDTRCKPIKASEAENV 133

Db 67 LDVK-NVSGIGQLDPMYTHSLDNLQNMIDTQACQYQVNVLSLCHTFLKSA----- 120
QY 134 SAIKPRREBFLSRMLMPDIDIMAYRGREVENNLPRLSAPGCCSRAPASGLSTPPA 193
Db 121 TVQPPG-----MP-----CNSTL---SLQSTL---TPDA 144
QY 194 SYEMSHLPVSSLL-PSDEFRDVRMVPANPFKERALPDQSRAPVGEYSRTTLEVPN 252
Db 145 TCVISSEYPPHLOEGSADQCKTIDESHF---HSPSVNHHNAGISKOAPPTSDG 200
QY 253 VC-----HSNIVSPKETTPEEARSDMHTSVAGELRPAASANAPYFPCDKASKEERP 306
Db 201 SCHELFPKQPNVYKLRNF-----YSKQYHKAAGPS-----QERVENQ 240
QY 307 ---SSEDEIATLHFEPPNAPLNKGLVSPQS-PQSDCCQNSPTEACSSKNACITLQASG 361
Db 241 FAEISTDTLTVESOPAVSHSECILESPEHLPSNFLAQPVNDSDHPBSDATCOQ----- 296
QY 362 PPAKSPDPKACMVKKYKFIVLNSLQNAKPGPEQALGRLSPRAYTAPAPACQPMPEP 421
Db 297 -PVQKRLKKAHLKLNLF-----LKSQRT---AEQVSEPK 328
QY 422 NLDIQSPYKLASGSDSTTPQASRLNNIVNRSMTGSPRSSSHSPLVMHPKCTSCGSG 481
Db 329 SDD--GLTKRLBASAKNTLEKAS-----SQ 351
QY 482 SPQHAEMCHTAQPTAEEMGEFTQSYSDSCENGAFFCNECQCRSEBASLKRHTLQTH 541
Db 352 SAEKE-----SEEV-----VSCEN--FNCSLSETEREDPALLEDQOTLQ 390
QY 542 SDRPYKCDRCQAFRYKGNLASHKVTYTGKPRYCNICGAQFNPANLKHTRHSGKP 601
Db 391 SQRQYAEELCGKPFKSNELHRSHTGKPRPCNCGHFSQAGLQTHLRHSGKP 450
QY 602 YKCEGAFVQVAHLRAVLIHTGEKPYCEICGTRFRHLQTLKSHLRHTGEKPYHCE 661
Db 451 YICEIGKGRPAASGDVQRHIIHSGEPRHICDLCGSGFSNFSNLKHKHTHMDXVFTCD 510
QY 662 KNLHFRHNSQLRLHQRHGAIITNTKVQYVSATDLPPLPAC 706
Db 511 ECGKSFNMQRKL-----VKRIHRTGERPYSCSAC 540

RESULT 12
US-09-107-058-9
Sequence 9, Application US/09107058
Patent No. US20010010922A1
GENERAL INFORMATION:
APPLICANT: Dalla-Favera, Riccardo
TITLE OF INVENTION: CLONING AND USES OF THE GENETIC
TITLE OF INVENTION: LOCUS bc1-6
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,058
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 0575/43771-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-107-058-9
MOLECULE TYPE: peptide

Query Match
Best Local Similarity 99.1%; Score 560; DB 3; Length 110;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 CIOFTHASDVLTNLRSLRDILTDVYIVVSREQFRAHKTVMACSGLFSIFTDQKLC 67
Db 1 CIOFTHASDVLTNLRSLRDILTDVYIVVSREQFRAHKTVMACSGLFSIFTDQKLC 60
QY 68 NLSVINLDEINPEGFCILLDPYTSRLNLRGNIMAVATMYQMERY 117
Db 61 NLSVINLDEINPEGFCILLDPYTSRLNLRGNIMAVATMYQMERY 110

RESULT 13
US-09-761-117-9
Sequence 9, Application US/09761117
Patent No. US20010012887A1
GENERAL INFORMATION:
APPLICANT: Dalla-Favera, Riccardo
TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS
TITLE OF INVENTION: bc1-6
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/761,117
FILING DATE: 16-Jan-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/43771-A-PCT-US-Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-761-117-9

Query Match
Best Local Similarity 99.1%; Score 560; DB 3; Length 110;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 2, 2006, 03:50:01 / Search time 43 Seconds
(without alignments)

1579.745 Million cell updates/sec

Title: US-10-755-889-18

Sequence: 1 MASPADSCIOFTRHNSVDLL.....TKVQYRVSAIDLPPELPKAC 706

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3793	100.0	706	2 A48752	B-cell CLL/Lymphom
2	3777	99.6	706	2 I52586	B-cell CLL/Lymphom
3	1151.5	30.4	480	2 JC7812	BCL6 homologous zi
4	602.5	15.9	794	2 S59069	Z13 protein - mus
5	552	14.6	688	2 A56360	myoneurin - human
6	522.5	13.8	610	2 JC7315	probable transcrip
7	501	13.2	673	2 S63336	transcription repr
8	495	13.1	595	2 G02075	gammaRBP-C - chick
9	491.5	13.0	676	2 I50643	hypothetical prote
10	491.5	13.0	701	2 T14757	zinc finger protei
11	479	12.6	693	2 I37570	zinc finger protei
12	478.5	12.6	1191	2 S35305	zinc finger protei
13	476	12.5	555	2 I53869	zinc finger protei
14	474.5	12.5	728	2 A48830	probable transcrip
15	468.5	12.4	428	2 A22831	zinc finger protei
16	468	12.3	803	2 S26823	zinc finger protei
17	463.5	12.2	710	2 I48668	zinc finger protei
18	460.5	12.1	686	2 A4612	zinc finger protei
19	454.5	12.0	469	2 I38600	knirpel-related p
20	453.5	12.0	427	2 A35659	finger protein zfp
21	453.5	12.0	553	2 S22954	finger protein zfp
22	450.5	11.9	209	2 A38073	transcription fact
23	446.5	11.8	519	2 A28073	transcription fact
24	445.5	11.7	466	1 TWFF	hypothetical prote
25	443	11.7	594	2 T12488	developmental cont
26	442.5	11.7	347	2 S00549	apertogenesis pr
27	442.5	11.7	580	2 A37107	finger protein OZF
28	442	11.7	292	2 S43826	finger protein mfg
29	441	11.6	169	2 A39240	

30	440.5	11.6	474	2 I54338	zinc finger protei
31	440	11.6	393	2 JN0533	finger protein pML
32	439.5	11.6	411	2 S10245	finger protein, te
33	438.5	11.6	651	2 B32891	finger protein 2,
34	437	11.5	201	2 I57505	zinc finger protei
35	436	11.5	576	2 A48157	renal transcrip
36	435	11.5	543	2 B34612	zinc finger protei
37	433.5	11.4	542	2 A54661	zinc finger protei
38	433.5	11.4	614	2 JH0500	zinc finger protei
39	432.5	11.4	475	2 S03679	hypothetical prote
40	432	11.4	386	2 T12527	hypothetical prote
41	429.5	11.3	455	2 T42670	finger protein HZF
42	428	11.3	247	2 S47070	finger protein - A
43	426.5	11.2	1350	2 S00647	zinc finger protei
44	424.5	11.2	325	2 I38616	zinc finger protei
45	423.5	11.2	675	2 S51037	zinc finger protei

ALIGNMENTS

RESULT 1
A48752
B-cell CLL/Lymphoma 6 (BCL6) protein - human
N/Alternate names: zinc finger transcription factor BCL-6
C/Species: Homo sapiens (man)
C/Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 01-Dec-2000
C/Accession: A48752
R/ye, B.H.; Lista, F.; Coco, F.L.; Knowles, D.M.; Offit, K.; Chaganti, R.S.K.; Dalla-Fa
Science 262, 747-750, 1993
A/Title: Alterations of a zinc finger-encoding gene, BCL-6, in diffuse large-cell lymph
A/Reference number: A48752; PMID:94053709; PMID:8235596
A/Accession: A48752
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-706 <YEA>
A/Cross-references: UNIPARC:UPI000016B151; GB:U00115; NID:G392426; PIDN:AAC50054.1; PID
A/Geneticis:
A/Gene: GDB:BCL6; BCL5; LA23; ZNF51
A/Cross-references: GDB:138176; OMIM:109565
A/Map position: 3q27-3q27
C/Superfamily: B-cell CLL/Lymphoma 5 protein; POZ domain homology
C/Keywords: transcription factor; zinc finger
F/18-121/Domain: POZ domain homology <POZ>
F/520-541/Region: zinc finger CCHH motif
F/548-568/Region: zinc finger CCHH motif
F/576-596/Region: zinc finger CCHH motif
F/604-624/Region: zinc finger CCHH motif
F/632-652/Region: zinc finger CCHH motif
F/660-681/Region: zinc finger CCHH motif

Query Match 100.0%; Score 3793; DB 2; Length 706;
Best Local Similarity 100.0%; Pred. No. 3,6e-218;
Matches 706; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MASPADSCIOFTRHNSVDLLNLRKRDILTDVIVVVSSEOPRAKTVLMACGLFYSI	60
DB	1	MASPADSCIOFTRHNSVDLLNLRKRDILTDVIVVVSSEOPRAKTVLMACGLFYSI	60
QY	61	FTDQKCNLSVINLDDPEINPEGCILDPMTSLNLRGIMAVMATMYLQMEHYVDI	120
DB	61	FTDQKCNLSVINLDDPEINPEGCILDPMTSLNLRGIMAVMATMYLQMEHYVDI	120
QY	121	CRKFTKSEAEVMSAIKPRPEEFNLSHMLPQDIMAAYRGVEVNNLPLRSAPGCSRAI	180
DB	121	CRKFTKSEAEVMSAIKPRPEEFNLSHMLPQDIMAAYRGVEVNNLPLRSAPGCSRAI	180
QY	181	APSLVSGSLTPPAISYMSHLPVSSLLFSDEERDVMPVAPNPPKRAIPCGSARVPVG	240
DB	181	APSLVSGSLTPPAISYMSHLPVSSLLFSDEERDVMPVAPNPPKRAIPCGSARVPVG	240
QY	241	EYSRPTLEVPNVVSHNIVSPKETIPREARSDMIVSAEGUKPAAPSAARNAPYPCDKAS	300
DB	241	EYSRPTLEVPNVVSHNIVSPKETIPREARSDMIVSAEGUKPAAPSAARNAPYPCDKAS	300

Db 241 EYSRPTLEVS PNVCHSNIVSPKRTIPEBARSDMHYSVAEGLKPAAPSAARNAPYPCDRAAS 300
 QY 301 KEERPPSSDEIATLHFEPPNAPLNKGLVSPQSPQSDCOQNSPTFACSSKNACTILOASG 360
 Db 301 KEERPPSSDEIATLHFEPPNAPLNKGLVSPQSPQSDCOQNSPTFACSSKNACTILOASG 360
 QY 361 SPPAPSPPTDPKACNMKKYKFIYVNSLNQNAKPGEGPQAEIGRLSPRAYTAPACOPMPMP 420
 Db 361 SPPAPSPPTDPKACNMKKYKFIYVNSLNQNAKPGEGPQAEIGRLSPRAYTAPACOPMPMP 420
 QY 421 ENLIDQSPPTKLSASGEDSTIPQASRLNNTVNSMTGSPRSSSESHSPLYMHPKCTSCGS 480
 Db 421 ENLIDQSPPTKLSASGEDSTIPQASRLNNTVNSMTGSPRSSSESHSPLYMHPKCTSCGS 480
 QY 481 OSPOHAEMLHTAGTFFAEEMGETOSEYSDSCENGAFFCNECDCEFSBASIKRHTTLOT 540
 Db 481 OSPOHAEMLHTAGTFFAEEMGETOSEYSDSCENGAFFCNECDCEFSBASIKRHTTLOT 540
 QY 541 HSDPKYKCDRCQASFFYKGNLASHKTVHTGEKPYPCNICGAQFNPANLKTHTRIHSGEK 600
 Db 541 HSDPKYKCDRCQASFFYKGNLASHKTVHTGEKPYPCNICGAQFNPANLKTHTRIHSGEK 600
 QY 601 PYKCTCGARFQVAHLRAHVLHTGEKPYPCNICGTRFRHLQTLKSHLRHTGEKPYHC 660
 Db 601 PYKCTCGARFQVAHLRAHVLHTGEKPYPCNICGTRFRHLQTLKSHLRHTGEKPYHC 660
 QY 661 EKCNLHFRHKSQRLRLRQKGAIITNTKQYRVSATDLPPELPKAC 706
 Db 661 EKCNLHFRHKSQRLRLRQKGAIITNTKQYRVSATDLPPELPKAC 706

RESULT 2

152586 B-cell CLL/Lymphoma 5 (BCL5) protein - human

N:Alternate names: finger protein LAZ-3; zinc finger transcription factor BCL-5

C:Species: Homo sapiens (man)

C>Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004

C/Accession: 152586; S40520; S32767

R/Hit1: T.; Kawamata, N.; Hirose, S.; Aoki, N.

Blood 83, 26-32, 1994

A/Title: Gene involved in the 3q27 translocation associated with B-cell lymphoma, BCL5.

A/Reference number: 152586; PMID:94100541; PMID:8274740

A/Accession: 152586

A>Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-706 <MIK>

A/Cross-references: UNIPROT:P41182; UNIPARC:UPI000012682C; GB:567779; NID:9459372; PIDN:

R/Kerker, J.P.; Dewelndt, C.; Tilly, H.; Quilef, S.; Lecocq, G.; Baastard, C.

Nature Genet. 5, 66-70, 1993

A/Title: LAZ3, a novel zinc-finger encoding gene, is disrupted by recurring chromosome 3

A/Reference number: S40520; PMID:9405122; PMID:8220427

A/Accession: S40520

A/Molecule type: mRNA

A/Residues: 1-706 <KEX>

A/Cross-references: UNIPARC:UPI000012682C; EMBL:Z21943; NID:9297025; PIDN:CAA79937.1; PI

C/Genetics:

A/Gene: GDB:BCL5, LAZ-3, ZNF51

A/Cross-references: GDB:125178; OMIM:151441; GDB:138176; OMIM:109565

A/Map position: 17q22-17q22; 3q27-3q27

A/Intons: 60/3

C/Superfamily: BRCORE-2 protein; POZ domain homology

C/Keywords: DNA binding; transcription factor; zinc finger

F/18-121/Domain: POZ domain homology <POZ>

F/520-541/Region: zinc finger CCH motif

F/548-568/Region: zinc finger CCH motif

F/576-596/Region: zinc finger CCH motif

F/604-624/Region: zinc finger CCH motif

F/632-652/Region: zinc finger CCH motif

F/660-681/Region: zinc finger CCH motif

Query Match 99.6%; Score 3777; DB 2; Length 706;
 Best Local Similarity 99.6%; Pred. No. 3, 2e-217;
 Matches 703; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MASPADSCIOFTRRASDVLTNLNRLRSRDIIITDVYIVYSREOFRAHKTIVLMAQSGLFYSI 60
 Db 1 MASPADSCIOFTRRASDVLTNLNRLRSRDIIITDVYIVYSREOFRAHKTIVLMAQSGLFYSI 60
 QY 61 FTDQKCNLSVINDPEINPBGCTILDPMYTSRLNLRGNIMAVMATMYLQMEHVYDT 120
 Db 61 FTDQKCNLSVINDPEINPBGCTILDPMYTSRLNLRGNIMAVMATMYLQMEHVYDT 120
 QY 121 CRKFKASBAEAVNSAIKPPREFLNSRMLMODIAVYGRFVENNLLPLRSAPGESAPF 180
 Db 121 CRKFKASBAEAVNSAIKPPREFLNSRMLMODIAVYGRFVENNLLPLRSAPGESAPF 180
 QY 181 APSLYSGISTPPASYSMTSHLPVSSLLPSDEEFRRVNPVNPFPKERRALPCDSARPVPG 240
 Db 181 APSLYSGISTPPASYSMTSHLPVSSLLPSDEEFRRVNPVNPFPKERRALPCDSARPVPG 240
 QY 241 EYSRPTLEVS PNVCHSNIVSPKRTIPEBARSDMHYSVAEGLKPAAPSAARNAPYPCDRAAS 300
 Db 241 EYSRPTLEVS PNVCHSNIVSPKRTIPEBARSDMHYSVAEGLKPAAPSAARNAPYPCDRAAS 300
 QY 301 KEERPPSSDEIATLHFEPPNAPLNKGLVSPQSPQSDCOQNSPTFACSSKNACTILOASG 360
 Db 301 KEERPPSSDEIATLHFEPPNAPLNKGLVSPQSPQSDCOQNSPTFACSSKNACTILOASG 360
 QY 361 SPPAPSPPTDPKACNMKKYKFIYVNSLNQNAKPGEGPQAEIGRLSPRAYTAPACOPMPMP 420
 Db 361 SPPAPSPPTDPKACNMKKYKFIYVNSLNQNAKPGEGPQAEIGRLSPRAYTAPACOPMPMP 420
 QY 421 ENLIDQSPPTKLSASGEDSTIPQASRLNNTVNSMTGSPRSSSESHSPLYMHPKCTSCGS 480
 Db 421 ENLIDQSPPTKLSASGEDSTIPQASRLNNTVNSMTGSPRSSSESHSPLYMHPKCTSCGS 480
 QY 481 OSPOHAEMLHTAGTFFAEEMGETOSEYSDSCENGAFFCNECDCEFSBASIKRHTTLOT 540
 Db 481 OSPOHAEMLHTAGTFFAEEMGETOSEYSDSCENGAFFCNECDCEFSBASIKRHTTLOT 540
 QY 541 HSDPKYKCDRCQASFFYKGNLASHKTVHTGEKPYPCNICGAQFNPANLKTHTRIHSGEK 600
 Db 541 HSDPKYKCDRCQASFFYKGNLASHKTVHTGEKPYPCNICGAQFNPANLKTHTRIHSGEK 600
 QY 601 PYKCTCGARFQVAHLRAHVLHTGEKPYPCNICGTRFRHLQTLKSHLRHTGEKPYHC 660
 Db 601 PYKCTCGARFQVAHLRAHVLHTGEKPYPCNICGTRFRHLQTLKSHLRHTGEKPYHC 660
 QY 661 EKCNLHFRHKSQRLRLRQKGAIITNTKQYRVSATDLPPELPKAC 706
 Db 661 EKCNLHFRHKSQRLRLRQKGAIITNTKQYRVSATDLPPELPKAC 706

RESULT 3

UC7812 BCL6 homologous zinc finger protein BAZF - human

C/Species: Homo sapiens (man)

C>Date: 03-Jun-2002 #sequence_revision 03-Jun-2002 #text_change 09-Jul-2004

C/Accession: UC7812

R/Sakshita, C.; Fukuda, T.; Okabe, S.; Kobayashi, H.; Hirose, S.; Tokuhisa, T.; Miyazawa, K.

Biochem. Biophys. Res. Commun. 291, 567-573, 2002

A/Title: Cloning and characterization of the human BAZF gene, a homologue of the BCL6 or

A/Reference number: UC7812; PMID:11855826; PMID:21845446

A/Accession: UC7812

A/Molecule type: DNA

A/Residues: 1-480 <SAK>

A/Cross-references: UNIPROT:Q6N143; UNIPARC:UPI0000072773; DBJ:AB076580; DBJ:AB076581

C/Comment: This protein, a zinc finger protein containing a conserved amino terminal BTE

ry in the induction of megakaryocytic differentiation to produce mature platelets. The

cell fate.

C/Genetics:

A/Gene: BAZF

A/Map position: 17p13.1

A/Intons: 60/2; 134/2; 256/2; 297/3; 353/1; 396/3; 442/3

C/Keywords: differentiation

Query Match	30.4%;	Score 1151.5;	DB 2;	Length 480;
Best Local Similarity	38.2%;	Pred. No. 2.8e-61;		
Matches 268;	Conservative 58;	Mismatches 142;	Indels 233;	Gaps 16;

[illegible]

RESULT 4

Z13 protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S59069
R:Schulz, T.C.; Hopwood, B.; Rathjen, P.D.; Wells, J.R.B.
Biochem. J. 311, 219-224, 1995
A:Title: An unusual arrangement of 13 zinc fingers in the vertebrate gene Z13.
A:Reference number: S59069; MUID:96003919; PMID:7575457
A:Accession: S59069
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-794 <SCH>
A:Cross-references: UNIPROT:060821; UNIPARC:UPI000016CAE7; GB:U14556; NID:g608136; PIDN:F10-108/Domain: POZ domain homology <POZ>

Query Match	Score	DB 2:	Length	794:
Best Local Similarity	25.7%	Pred: No. 2-2e-26;		
Matches 194;	Conservative 100;	Mismatches 284;	Indels 177;	Gaps 23;

```

OY 1 QGFRRHSDVLTMLNTRLSRSDILTDVYIVYSREBQFRAHKTUVMASCSGLFYSIFPDQJCN 68
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MDPFQSHQRYVEOLNQRQGLCLDCSTCFVVDGVDFKHAKVLAACSYFYKLPVDO----- 56

OY 69 LSVNLDPENBEGFCILDFMYTSRLNREGINAMVATMYLQMEHVVDTCRKF1KAS 128
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 57 KDVVHLDIS -NAGLGGVLEFMYTAKLSLSPENDDVLAVASFLQOMDI V1ACHTTLKSLA 115

OY 129 EAEVWSAIKPPREFLSRMLMPQDIWAYKREVENNLP1RSAPGCEBFAFASLYSGL 188
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 116 EPSSTTG-----ESADASAEEGDOKA----- 137

OY 189 STPASYSMYSHLPVSSILFSDSEFRDVRMPVANPPEKRALPCDSA-----BPVP 239
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 138 KDEKAAATMLSRLOAQAGSSSTGCRELK-----EENGGQAEBSASSGAEQTEKADAF 189

OY 240 GEYSRPTLEVASPNVCHSNITYSPKETTIDEBARSDMHYSVAEGLKPADAPBANNAPYPCDCA 299
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 190 RE--PPPELKPDPDTSSMAAEALSSBSQEW-----VEBASKE-----DQ 233

OY 300 SKEEBRSEDEETALHF---EPRAPLNRGLVSPQSPKSDCQPNSPTEACSSNNACIL 356
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 234 EEEGAGPATVYEBGWHLDNGEPRENEBSAATDSGQELGMEGONILRSTGYDRTES----- 289

OY 357 QASGPPAKSPTDPKACNMWKYKUTVLNLSLQNKPPGGPEOAE1GRLSPRAYTAPPAQ- 415
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 290 KAYGGI1HK-----CEDCGKETTHGNFGRH1RIHTEGEPFRCBESKAFSPDPAACKA 342

OY 416 -----PMEPENLLOSPFTKLSAGBDSST1PQASRLN1NVRSMTGSPRSSSESHSLYM 470
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 343 HEKTHSPLKPYGCE-----ECGKSRYLSILN---LHKRHSHGEARY----- 381

OY 471 HPPKCTSG-----SGSPQHAEMC1HTAAPTAR-----EMGETQ 505
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 382 ---RGGDGSKLFTTSGNLKRHLVHSGKPYQCYC---GRSFSDP1RSKRNH1ETHD1D 434

OY 506 SEYSDSCB-----NGAFCECDECRFSFEASLAKHTLQ1TSH-DKPY 546
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 435 KEHKCPHCDKPKFNOVGNLKAHLK1H1ADGPLKCRBQCGQFTTSGNLKRN-LR1HSGEKPY 493

OY 547 KCDRCQASPRYKGNLASHKTVHTEGKPYRNC1CGAOFNRPA1LK1THTR1HSGEKPYKSET 606
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 494 VCHNQRFADPBGALQRFVRL1HTEGKPYCQV1ICGKAFQASSL1AHVQH1TEGKPYUCBER 553

OY 607 CGARFVQVLAH1RANVL1HTEGKPYCE1CGRFR1LOTLKSH1R1HTEGKPYHCKSM1H 666
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 554 CGKRFVQSSOLANH1R1HDK1RPDKCSVCSKAFVNVGDLSKH11HTEGKPYL1CDKCGRG 613

OY 667 FRHKSQ1RLH1ROKGA1TNTK1QVRYVATD1LPE 701
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 614 FNRVNL1RSHV1T1HOGKAG1KI-----LEPE 640

```

RESULT 5

zinc finger protein (clone 18) - human
N/Alternate names: GLI-related finger protein HKR3
C/Species: Homo sapiens (man)
C/Date: 03-Oct-1995 #sequence_rev10on 03-Oct-1995 #text_change 09-Jul-2004
C/Accession: A56360; E31201
R:Sugawara, M.; Scholl, T.; Ponath, P.D.; Strominger, J.L.
Mol. Cell. Biol. 14, 8438-8450, 1994
A/Title: A factor that regulates the class II major histocompatibility complex gene DPA
A/Reference number: A56360; MUID:95059073; PMID:7969177
A/Accession: A56360
A/Molecule type: mRNA
A/Residues: 1-668 <RUG>
A/Cross-references: UNIPROT:P10074; UNIPARC:UPI00016B34F; GB:L16896; NID:G292934; PIDN:
R.huppert, J.M.; Künzler, K.W.; Wong, A.T.; Bigner, S.H.; Kao, F.T.; Law, M.L.; Senanez
Mol. Cell. Biol. 8, 3104-3113, 1988
A/Title: The Gli-Kruppel family of human genes.
A/Reference number: A93103; MUID:89096896; PMID:2850480

A:Accession: E31201
 A:Molecule type: DNA
 A:Residues: 461-516 <RBP>
 A:Cross-references: UNIPARC:UPI000017C425
 C:Genetics:
 A:Introns: 506/1
 A:Note: the list of introns may be incomplete
 C:Keywords: DNA binding; zinc finger
 P:12-111/Domain: POZ domain homology <POZ>

Query Match 14.6%; Score 552; DB 2; Length 688;
 Best Local Similarity 25.0%; Pred. No. 1.9e-25;
 Matches 190; Conservative 104; Mismatches 269; Indels 196; Gaps 28;

```

QY 11 FTRHADVLTNLRSLRDLTDVIVVSRGPRAKTYLMACSGLYSIFTDQLKCNIS 70
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 5 FVCHSVRVVLOELNKKOREKQYCDATLDVGLVFKAMSVLACCSHFOSLYGGSGSV- 63
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 71 VINLDEINDEGFC---ILLDMYTSRLNREGNIMAWATAMVLOMEHVDTCKRFYK 126
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 64 -----VLPAGPAETFGILLDFPYTGHLALTSGNDQVLLARRELVRPAVELCOSF-- 114
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 127 ASEAEVSAIKPRREFEFLNSRMLMPDIMA YRGREVENNLPLRSAPGCESSRAFA SLYS 186
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 115 -----KP-----KTSVGOAAGG-----S 128
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 187 GLSTPPASYSMTYHLVSVSLIFSDDEFRDVRMVPANPFKERALPCDSARPVGERSRPT 246
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 129 GLG-PPASQVNSHVKEPAGLEEEVSRITGL-----VPRDQ-PPGSHSP-----QRRQ 176
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 247 LEVSPVNCNSNIYSPKETIPBEARSDMHVSAEGLKRAA-----PSARNAVPFCDKASK 301
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 177 L-----HSPAS--EGPSSLCGKTKQALPFCSEDKKPEDCKTPRPLEBGA 222
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 302 EBERPSEDEIALHFE-----PNAFLNRKGLVSPQSPKSDCQPNPTACSSKX 352
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 223 QLGGSNEMEVVVVQVEDDGDGYSVMESEAVLTR-----KSNVIRKPCAAER 269
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 353 ACTLOAGSGPPAKS-----PTDPKACNMK--KTYFVILNSLNQNAKPGEPQALGRL 403
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 270 ALSAGSILAEPAENRKGTA VAVPCPTCHKKFLSKYLLKVNRRKHTGSKP----- 318
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 404 SPRAYTAPRACQPRMEBENDLOSPTKLSASGEDSTIPQASRLNNTVNSMTGSP----- 458
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 319 -----FECPCCKGCKYFRKKNL-----LHLEAR--NCKNRSEQVLLPCSVCO 356
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 459 ---RSSSESHSPLYMH---PRCTSGSGSPQHAEMCIHT-----AGPTPAE-E 500
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 357 ETRRRRLMELAVHNVSHTGEMPRYKSCSGSQPMQKXOLDSMILHGAPKPHACPTCAKCP 416
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 501 MGETQSEYSDSCENG--AFPCNECDRFSSEASLKRHTLTQTH-SDKPYKCDRCQASFRY 557
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 417 LSRTEILOHBAFGRGKFLFVCECGHRASSRNGLOMHIKAKRNRNEPHECFCSHAFTQ 476
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 558 KGNLASKYTHNGEKPRKCNICGAQFNRPA NLKTHIRISGEKPYKCEGTGAFVQVANH 617
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 477 KANLNMHLRTHTEBKRPOCHLCKGTFTQASLDKRNKTHGERPFSECFEORFTEGRL 536
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 618 RAHVLI-HTGEKPYCEICGTRFRHLQTLKSHLRHTGEKPYCEKCNLFRKKSQRLRL 676
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 537 LRHVASHHGGRHPRFOICGKTFRVAVQLVHVRHNGVAKKFGCTEGCYFTQAHLLRH 596
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 677 LRQHGAIYTKVQYR-----VSATDLPEEL 702
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 597 M-EIHDRVENYKPRORLRLIIEDEKVVVALQPAEL 634
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

RESULT 6

UC7315
 myoneurin - human
 C:Species: Homo sapiens (man)
 C:Date: 08-Sep-2000 #sequence_revision 08-Sep-2000 #text_change 09-Jul-2004
 C:Accession: UC7315

R:Alliel, P.M.; Seddigi, N.; Goudou, D.; Cifuentes-Diaz, C.; Romero, N.; Velasco, E.; Ri
 Biochem. Biophys. Res. Commun. 273, 385-391, 2000
 A:Title: Myoneurin, a novel member of the BTB/POZ-zinc finger family highly expressed in
 A:Reference number: UC7315
 A:Accession: UC7315
 A:Molecule type: mRNA
 A:Residues: 1-610 <ALL>
 A:Cross-references: UNIPROT:Q9NPC7; UNIPARC:UPI000000D72A; GB:AF14884
 C:Comment: This protein, belonging to the family of eukaryotic BTB/POZ and zinc finger p
 and a regulator in the genital tract.
 C:Keywords: tandem repeat; transcription regulation; zinc finger

Query Match 13.8%; Score 522.5; DB 2; Length 610;
 Best Local Similarity 23.9%; Pred. No. 9.4e-24;
 Matches 170; Conservative 79; Mismatches 208; Indels 255; Gaps 21;

```

QY 9 IQFTRHADVLTNLRSLRDLTDVIVVSRGPRAKTYLMACSGLYSIFTDQLKCN 68
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MQVSHHCEHLERLNKQREAGFLCDCTIVTGFQFKARHNVLASFSYGAIGYSTSENN 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 69 LSVINLD-PEINPBGFCILLDMYTSRLNREGNIMAWATAMVLOMEHVDTCKR 122
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 ---VFLDSQVADGFQKLEFIYGTNLDSMNKKEIHQADVLYKVEVTKCKIKED 117
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 123 -KFKASEAEVSAIKPRREFEFLNSRMLMPDIMA YRGREVENNLPLRSAPGCESSRAFA 181
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 118 PAFIANPSTETSSITGNIE--LNQOTCL-----LTLRD----- 149
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 182 PELYGLSTPPASYSMTYHLVSVSLIFSDDEFRDVRMVPANPFKERALPCDSARPVG 241
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 150 -----YNNREKSEVSTDLIQANPKGAL----- 172
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 242 YSRPTLEVPVNCNSNIYSPKETIPBEARSDMHVSAEGLKRAAASARNAVYFPCDKASK 301
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 173 -----AKTSQ 178
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 302 EBERPSEDEIALHFEPPAPLNRKGLVSPQSPKSDCQPNPTACSSKNAIILQASGS 361
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 179 TKKKKKA-----FNSPTGQNK--TVQYR--SDILENASVELFLDAN----- 216
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 362 PPAKSPDPKACNMWKYKTFVILNSLNQNAKPGEPQALGRLSPRAYTAPRACQPRMEBE 421
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 217 ---KLPT-----PVEGVAQIN-----D 231
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 422 NLDLOSPTKLSASGEDSTIPQASRLNNTVNSMTG--SPRSSSESHSPLYMHPRCTSGC 479
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 232 NSELE-----LTSVVENTPRAODIVHTVTVKRRGSOQNCALKEHS-----MSNIAS 279
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 480 SOSPOHAEMCLHTAGPTFAEEMGETQSEYSDSCENGAFPCNECDRFSSEASLKRH--- 536
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 280 VKSPTYEA-----NSGEELDQRYSKAP-----MCTTCGKVFEASLSRRHMTI 323
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 537 -----TLQTH-----SDKPYKCDRCQASFRYKGNLASHKTVHTG- 570
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 324 HGVKPYVCHLGKAFQTCNQCKTHVTRHTGKPYKCELCIDGFAQCKQLVPHSRMHGE 383
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 571 EKPYRKNICGAQFNRPA NLKTHIRISGEKPRKCNICGAQFNRPA NLKTHIRISGEKPY 630
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 384 EKPYKDVCNLQFAVSSNLIKARHSGEPRVYCDRCQGFQVQASGLTVYVNRHNGEKPY 443
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 631 PEICGTRFRHLQTLKSHLRHTGEKPYCEKCNLFRKKSQRLRLRQKHG 682
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 444 VCDTCKAPAVSSSLTHSRKHTGKPYTCGLGKSFISGGLNGHFRSHTG 495
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

RESULT 7

S36336
 probable transcription factor PLZF - human
 C:Species: Homo sapiens (man)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 C:Accession: S36336; S31989
 R:Chen, Z.; Brand, N.J.; Chen, A.; Chen, S.J.; Tong, J.H.; Wang, Z.Y.; Waxman, S.; Zeller
 EMBO J. 12, 1161-1167, 1993

C:Superfamily: BRcore-2 protein; POZ domain homology
F:49-152/Domain: POZ domain homology <POZ>

Query Match 13.0%; Score 491.5; DB 2; Length 676;
Best Local Similarity 26.0%; Pred. No. 7.4e-22;
Matches 175; Conservative 81; Mismatches 245; Indels 173; Gaps 29;

```
QY 14 HASDVLTINLRSLRDLTDVIVVSRBQRAKTVLMACSGLFYSIFTDQKCNLSVYN 73
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 45 HSGQLIQNTQRTKGFCDVITVQNALFRAHKILTAASAVLKSLVYND-----NLIN 99
QY 74 LDPE-INPQGFCLLDFTMTSLNLT-----REGNIMAVMATYMTQMEHVVDTCRKFIKAS 128
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 100 LDHEWVSPGIFRIILDFITGRIGCBQPGEGSIGVLAASVYLQIRGLVLCCKKTLK-- 157
QY 129 EAEVSAIRPPREFLSKRLMEQDIMAIRGREVVENNLPKSAPEGSEK-AFAP-SLYS 186
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 158 -----RSGKYCHLRGGVAPYKLR 176
QY 187 GL-STPPASVMSYSHLPVSSLLFSDDEPRDYRMVANPPKBRALPCDSARPVPGESRP 245
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 177 GLRATTPVIQACTSGTP-----RPVDLQ-----PVEPAADLNTQ---CGELVYS 217
QY 246 TLEVSFNVCHSNITSPEKTIPEERASDMYSVAEL-----KPAADANAPYPCDKAS 300
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 218 ASQGT--LHPHGLCPPE-----RHCSPPCGLDLSKSPGSAQ---LIPTRDLL 263
QY 301 KEERPSSEDEIALHFEPP--NAPLNKGLVSPQSKDCQONS-----PTACSSK 351
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 264 PAEPREPS-----LPPRHDSPPVSGILAGHPAAYDSPGSGHPGHPHATDFRS-- 314
QY 352 NACILQASSPPAKSPPTDPA-----CMWKYKFFVLSNLSNNAKRPGR--EQALGL 403
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 315 -----TPPAEPPLPRGDRBELMTRMKH-----PFLGYLDEGEAEK 353
QY 404 SPRAVTA--PPACOPMER--ENILDIQSPTKLASAGEDSTIIPQ--ASRLNNIVRSMTGSP 458
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 354 LEEEEKABSPRAPQRRYVSVEBNDELPNDSIEEFGSSBGRPGALRYCNH--LGYP 412
QY 459 RSSSEHSPLVMHPRYCTSGSOSPOHAEMCLHTAGPTAEEMGETQSEYSDSSCENGAF 518
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 413 ESTGDN---LYV---CIPCGKGFPSSEQLNAHV-----EAMNEEELYHKKAAEQAVP 458
QY 519 FQNECCORFSEESLKRHTLQTHSDKPRYCDRCQASFRYKSNLASIKYTHGKPRCVI 578
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 459 FLDKGGAGLGDII-----RPRYCSCKSYKDPATLRQHEKTHMLTRPPCTI 506
QY 579 CGAQFNRPANLKTHTRIHSGEKPYKCECTGAFVQVAHLRAVLIHTGEKPYCEICGR 638
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 507 CGKKTQRCGTMTNHSLSLQKRFACDACGMRTTQRYRLTEHRIHSGEKPYECQVCGAK 566
QY 639 FRHLQTLKSHLRTH 652
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 567 FAQQRNLTISHMKW 580
```

RESULT 10

T14757
hypothetical protein DKFZp572C163.1 - human (fragment)

C:Species: Homo sapiens (man)
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T14757
R:Submitted: R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, August 1999
A:Reference number: Z18181
A/Accession: T14757
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-701 <MAN>
A:Cross-references: UNIPROT:Q9UG02; UNIPARC:UPI00006DDA3; EMBL:AL110217
A:Experimental source: adult subthalamic nucleus; clone DKFZp572C163
C:Genetics:
A>Note: DKFZp572C163.1

C:Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology

Query Match 13.0%; Score 491.5; DB 2; Length 701;
Best Local Similarity 40.6%; Pred. No. 7.7e-22;
Matches 91; Conservative 30; Mismatches 86; Indels 17; Gaps 3;

```
QY 472 PPKTSCGSQSPQHAEMCLHT-----AGPTAEEMGETQSEYSDSSCENG-----A 517
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 467 PVECNQCGKTFPQQRHLCHQRILHTGEKPYECNECGKT---PADSALRAHRIHTGEK 523
QY 518 FQNECDCKFSEASLKHHTLQTHSDKPYKCDRCQASFRYKSNLASIKYTHGKPYRCN 577
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 524 YECNDCKGTFPSKTHSLRAHLTRSGEKPYECSECKTFSEKSYVASAQRVHTGEKPYECN 583
QY 578 ICGAQNRPANLKTHTRIHSGEKPYKCECTGAFVQVAHLRAVLIHTGEKPYCEICGT 637
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 584 YCGKPFANSTLRVQRILHTGEKSYECNDCKGTFPQKHLSHQRILHTGEKPYECNECGK 643
QY 638 FRHLQTLKSHLRTHHTGEKPYKCECNLHFRKSOQLRLHROKH 681
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 644 AFAQNSTLRVQRILHTGEKPYECDECGKTFVAKALRYVHTRMH 687
```

RESULT 11

137570
zinc finger protein - human (fragment)

C:Species: Homo sapiens (man)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C/Accession: I37570
R:Submitted: M.; Aveskog, M.; Hellman, L.
DNA Cell Biol. 14, 125-136, 1995
A>Title: Isolation of cDNA clones for 42 different Kruppel-related zinc finger proteins
A:Reference number: I37566; MIMD:95169271; PMID:7865130
A/Accession: I37570
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-693 <RES>
A:Cross-references: UNIPROT:Q14588; UNIPARC:UPI000016AACB; EMBL:X78927; NID:9498726; PTD

C:Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology

Query Match 12.6%; Score 479; DB 2; Length 693;
Best Local Similarity 28.5%; Pred. No. 4.2e-21;
Matches 141; Conservative 61; Mismatches 188; Indels 104; Gaps 17;

```
QY 195 YSMYSHLPVSSLLFSDDEPRDYRMVANPPKBRALPCDSARPVGEYSRPTLEYSFNV 254
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 208 FQSSHLLQTHQVHT-----VEKPF-----KVECGK-----GFSRSTLV----- 244
QY 255 HSNITSPKE--TIPEARDMAYS-----VAGLKPAAASARNAAPYPCDKASKKEER 305
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 245 HCKLHSGEKPYNCECGRAFIASHLOEORILHTGEK-----FKDTCGKNFR 294
QY 306 PSEDEIALHFEPPAPLNKGLV--SPQSPQSDQPNSPTEACSSKNACTLDA---SGSP 362
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 295 RSA-----LNNHCMTHTGEKPYK--CEDCGKCTCSS--NLRHQRVHTGK 337
QY 363 PAKSPTDPAKCMWKYKFFVLSNLQNAKPGGPEQALIGRLSPRAVTAAPACOPMERPN 422
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 338 PPKCECGK--CTIQSQQAHRIHTGEKPYKCYGKGFISSSFOAHQVHTG----- 391
QY 423 LDQSPTKIASAGEDSTIPQASRLNNIVRSMTGSPRSSSEHSPLVMHPRYCTSGSOS 482
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 392 ---EKPYKNECGKSFMRKIHVQVHLVH---TGE-----KPYKCEVCGKAF 432
QY 483 PQHAEMCLHTAGPTAEEMGETQSEYSDSSCENGAFQNECDCKFSEASLKHHTLQTHS 542
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 433 RGSSTLKTLKHAHSVOK-----DPKCECGQGFNQSSRLDIHQILHTG 475
QY 543 DRYKCDRCQASFRYKSNLASIKYTHGKPYRCNIGCAQFNRPANLKTHTRIHSGEKPY 602
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 476 EKPYPKCECGKGFNRADLKHCRILHTGEKPYNCECGKVFSQAHLTLTHQVHSGEKPF 535
```

QY 603 KCETCGARFVQVAHLRAVLHTGKPYPCICGTRFRHLQTLKSHLHTGKPYHCEK 662
 Db 536 KCECECKSFGRSAHLQAHQVHTGKPYKCGECGKPFKMSLNDMQRVHTGKPYTCGA 595
 QY 663 CNLHFRHKSQTLRH 676
 Db 596 CGKHFSQASSLQLH 609

RESULT 12

S35305
 zinc finger protein ZNF91 - human
 C:Species: Homo sapiens (man)
 C:Date: 31-Dec-1993 #sequence_revision 02-Jun-1994 #text_change 09-Jul-2004
 C:Accession: S35305
 R:Belletrou, E.J.; Marine, J.C.; Ried, T.; Leococq, P.J.; Riviere, M.; Amemiya, C.; Pond
 EMOU J. 12, 1363-1374, 1993
 A:Title: Clustered organization of homologous KRAB zinc-finger genes with enhanced expe
 A:Reference number: S35305; MUID:93223677; PMID:8467795
 A:Accession: S35305
 A:Molecule type: mRNA
 A:Residues: 1-1191 <BEL>
 A:Cross-references: UNIPROT:Q05481; UNIPARC:UP1000013C42A; EMBL:L11672; NID:g186773; PII
 A:Note: the authors translated the codon GCA for residue 750 as Thr and GCT for residue
 C:Genetics:
 A:Gene: GDB:ZNF91; HEP7; HEP10
 A:Cross-references: GDB:132284
 A:Map position: 19p12-19p12
 C:Keywords: DNA binding; zinc finger

Query Match 12.6%; Score 478.5; DB 2; Length 1191;
 Best Local Similarity 38.1%; Pred. No. 8.4e-21;
 Matches 96; Conservative 26; Mismatches 91; Indels 37; Gaps 5;

QY 472 PPKCTSGSGSPQHAEMCLHTAGPTFAEMGETOSEYSDSSCENGAFPCNECCRSEBEA 531
 Db 909 PYKCECGKAFSOPSHLTTH-----KRMHTGKPYK-----CECGKAFSOS 951
 QY 532 SLKRLTLQTHSDKPYKCDRCQASFRYKGNLASHHTVHTGKPYKCNICGAQFNRPANLTKT 591
 Db 952 TLTLTKHIIHTGKPYKCECGKAFKRSSTLTENKIIHTGKPYKCECGKAFSOSSTLTR 1011
 QY 592 HTRHISGEKPYKCTCGARFVQVAHLRAVLHTGKPYPCICGTRFRHLQTLKSHLRI 651
 Db 1012 HTRHHTGKPYKCECGKAFKRSSTLTENKIIHTGKPYKCECGKAFISSTLTNGHRI 1071
 QY 652 HTGKPYHCEKCNLHFRHKSQTL-----RLHFRQK-----HGATNTVQYRVS 694
 Db 1072 HTRKPYKCECGKAFSOSSTLTENKIIHTGKPYKCECGKAFKRSSTLTNGHRI 1128
 QY 695 ATDLPELPKAC 706
 Db 1129 TGEKPYKCEKC 1140

RESULT 13

153869
 zinc finger protein - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
 C:Accession: 153869
 R:Brady, J.P.; Piatigorsky, J.
 Gene 149, 239-304, 1994
 A:Title: A mouse cDNA encoding a protein with zinc-fingers and a KRAB domain shows simi
 A:Reference number: 153869; MUID:95047492; PMID:7959006
 A:Accession: 153869
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-555 <RBS>
 A:Cross-references: UNIPROT:O6218; UNIPARC:UP1000002920B; GB:L28167; NID:g758660; PIDN:
 C:Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology

Query Match 12.5%; Score 476; DB 2; Length 555;
 Best Local Similarity 28.0%; Pred. No. 4.9e-21;
 Matches 134; Conservative 53; Mismatches 190; Indels 102; Gaps 14;

QY 277 VAEGLKPAAPSAARNAFYF-----PCDKASKEERPSSEDE-----IALHF-EPPNAP 322
 Db 102 VTDDLFTSQNSVNTQLOQKAPC-QSRPRPAPAVSDENYIKSHITISVPIHSGRPLPT 160
 QY 323 LNRKGL-VSPQSFQSDCCPNPTEACSSKACILQASGSPKASPTPRKACWKKKYKFI 361
 Db 161 LRAQSTSLTERQTRKQYHQSHRDAGQRKRESHTSWIPRPS--DHRVCKSK----- 213
 QY 382 VNSLNQNAKPGPEQAEIGRLSPRAYTAAPACQPMPEBNLDLQSPTKLSAGSDSTIP 441
 Db 214 -----GRCSPSHGDDGVVFPD-QNGSIHTRQSSQIREAVT-- 251
 QY 442 QASRLNNIVRSMWTSPPRSSSHSPLYM--HPKCTSGSGSPQHAEMCLHTAGPTFAE 499
 Db 252 -----DLSSDPHQVLDGGGRACACVCEGGRGSPCGTDCIHGGRTGEE 295
 QY 500 --EMGETQ-----SEYSDSSCENG-----AFPCNECCRSEBEASLK 534
 Db 296 RKEFGHQVCTPYKPYTCQCEKSLVDQHLMSHVHTREPRYNGETCGSARFQASHQ 355
 QY 535 RHTLQTHSDKPYKCDRCQASFRYKGNLASHHTVHTGKPYKCNICGAQFNRPANLTKTHT 594
 Db 356 DHQRLHTGKPYKCDRCQASFRYKGNLASHHTVHTGKPYKCNICGAQFNRPANLTKTHT 415
 QY 595 IHSGEKPYKCTCGARFVQVAHLRAVLHTGKPYPCICGTRFRHLQTLKSHLRIHTG 654
 Db 416 VHTGKPYKCDRCQASFRYKGNLASHHTVHTGKPYKCNICGAQFNRPANLTKTHT 475
 QY 655 EKEPYHCEKCNLHFRHKSQTLRLH-----QNGAITNTVQYRVSATDL 699
 Db 476 EKPYSCDVCGKGFGRSSQLQSHQVHTGKPYKCDRCQASFRYKGNLASHHTVHTGKPYK 534

RESULT 14

A48830
 probable transcription regulator NT fin12 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C:Accession: A48830
 R:Noce, T.; Fujiwara, Y.; Ito, M.; Takeuchi, T.; Hashimoto, N.; Yamamouchi, M.; Higashi
 Dev. Biol. 155, 409-422, 1993
 A:Title: A novel murine zinc finger gene mapped within the tw18 deletion region express
 A:Reference number: A48830; MUID:93162306; PMID:8432396
 A:Accession: A48830
 A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-728 <NOC>
 A:Cross-references: UNIPROT:Q06054; UNIPARC:UP100000273C3; GB:D10632; NID:g286104; PIDN
 A:Experimental source: testis
 A:Note: sequence extracted from NCBI backbone (NCBIN:124763, NCBIN:124765, NCBI:P.124766
 C:Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology

Query Match 12.5%; Score 474.5; DB 2; Length 728;
 Best Local Similarity 25.6%; Pred. No. 8.2e-21;
 Matches 134; Conservative 64; Mismatches 189; Indels 137; Gaps 13;

QY 255 HSNLYSPKETIPPE-----ARSDMHSVAGLKPAAASARNAFYFPCDKA 299
 Db 169 YSSLYRHRRTYHPEKPYKLTENCKNSILYLHKKVHVIHIGEK-----YKLTIC 218
 QY 300 SKKEERSSDEIALHPEPNAPLNRKGLVSPQSFQSDCCPNPTEACSSKACILQAS 359
 Db 219 GKCYTHSSFEKHTRIHE-----ESYKCNDRKSP-----ICCGGLK 256
 QY 360 GSPPAKSPDPAKCNMKKYKFTVLSLNQ-----ARQGEQAEIG 401
 Db 257 RHHHTHGEKPYKCDRCQASFRYKGNLASHHTVHTGKPYKCNICGAQFNRPANLTKTHT 316
 QY 402 RLSPRAYTAPACQPMPEBNLDL-----QSPTKLSAGSDSTIPQASRLNNIVRSM 454

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Db      317 HNGEKAYICAECKKCFIQSKLTHQRIHTGEKSYKCSBCKSFYVGSSLRIT--QRIT 373
QY      455 TGSPPRSSSSSHSLYVHPKCTISCGSQSPQHAEMCLHTAGPTFAEMGETQSEYSDSCE 514
Db      374 TGE-----KPYKSCCHCKCFIQAHLRH-----QKIHTEKPKYKSCBCE 413
QY      515 NG-----AFPCNECDRPFSEASLKRHTLOTNSDKPYKCDRCQASFR 556
Db      414 KSEFTVSDLRMHOKITGEKPYKSCDCKCFIQAKLKHQRIHTGEKPKYKSCBCKCF 473
QY      557 YKGNLASHKTVHTGEKPYKCNICGAQFNRPANLKTHTRIHSGEKPYKCECTGAFVQVAH 616
Db      474 VVSDLATHTQKIHTEKPKYKSCDCKCFIRKANLRHRHRIHTGEKPKYKSCDCKCFIQKAN 533
QY      617 LRAHVLHTGEKPYKCEICGTRFRHLQTLKSLRIHTGEKPKYKCNLHFRHKSQRLH 676
Db      534 LRTHRIHTGEKPKYKCB-CGKSFYVGSDLRKHQKCHTGEKPKYKSCBCKCFIRKALRRH 592
QY      677 LR-----QKHGALTNTKVQ-----YRVSATD 697
Db      593 QRHTGEKPKYKSCDCKCFIQKANLRTQKIHTEKPKYKSCBD 636

```

RESULT 15

```

A32891
finger protein 1, placental - human
C/Species: Homo sapiens (man)
C/Date: 20-Oct-1989 #sequence_revision 20-Oct-1989 #text_change 09-Jul-2004
C/Accession: A32891
R/Bellefroid, E.J.; Lecocq, P.J.; Benhida, A.; Poncelet, D.A.; Belayew, A.; Martial, J.A.
DNA 8, 377-387, 1989
A/Title: The human genome contains hundreds of genes coding for finger proteins of the K
A/Reference number: A32891, M01D:89377476, PMID:2505992
A/Accession: A32891
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-428 <BBL>
A/Cross-references: UNIPROT:PS1522; UNIPARC:UPI000013C426; GB:M27877
C/Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology
C/Keywords: tandem repeat

```

```

Query Match      12.4%; Score 468.5; DB 2; Length 428;
Best Local Similarity 41.0%; Pred. No. 1e-20;
Matches 96; Conservative 26; Mismatches 77; Indels 35; Gaps 6;

QY      459 RSSSESHSLYM--HPPKCTSCG-----SQSPQHAEMCLHTAGPTFAEMGETQSEYSD 510
Db      45  KSNLASHQRIHTGEKPKYKCNCGKVFHNSHLAQHRR--IHT-----GEK----- 87.

QY      511 SSCENGAFFPCNECDRPFSEASLKRHTLOTNSDKPYKCDRCQASFRYKGNLASHKTVHTG 570
Db      88  -----PYKCNCGKVFNOISHLAQRIHTGEKPKYKCNCGKVFQISHLAQRIHTG 141

QY      571 EKPRCNICGAQFNRPANLKTHTRIHSGEKPYKCECTGAFVQVAHLRAHVLHTGEKPY 630
Db      142 EKYECKKCKGKVSNSYLVOHLIHTGEKPYKCNVCGKVFHNSHLAQHRIHTGEKPY 201

QY      631 PCIECGTRFRHLQTLKSLRIHTGEKPKYKCNLHFRHKSQRLHRLRQK 680
Db      202 KNCBCKGVFSHKSSLVNHWRIHTGEKPKYKCNCGKVFSHKSSLVNHWRIHTGEK 255

```

Search completed: March 2, 2006, 03:54:29
Job time : 46 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 2, 2006, 03:45:47 ; Search time 187 Seconds
(without alignments)
1658.831 Million cell updates/sec

Title: US-10-755-889-18

Sequence: 1 MASPDSCICQTRHNSVDLL.....TKVQKRVSAITDLPPELPKAC 706

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*
- 9: Geneseqp2005as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3793	100.0	706	3 AAY78793	Aay78793 Human BCL
2	3793	100.0	706	4 AAB29640	Aab29640 Human bcl
3	3793	100.0	706	8 ADL82847	ADL82847 Human PRO
4	3793	100.0	706	8 ADL82847	ADL82847 Human PRO
5	3793	100.0	706	9 ADY19590	ADY19590 PRO polyP
6	3777	99.6	706	8 ADY14065	ADY14065 Human NF-
7	3777	99.6	706	9 ADY15006	ADY15006 PRO polyP
8	3771	99.4	706	7 ADY70182	ADY70182 Human hea
9	3763	99.2	706	2 AAR68743	Aar68743 BCL-6 zin
10	3763	99.2	706	3 AAY78792	Aay78792 Human BCL
11	3602.5	95.0	707	5 ABB57289	Abb57289 Mouse lsc
12	1158.5	30.5	458	8 ABM84710	Abm84710 Human dia
13	1155	30.5	479	6 ABU03467	ABU03467 Angiogene
14	1155	30.5	479	7 ABU64323	ABU64323 AAC2-2 pr
15	1155	30.5	479	7 ADN38698	ADN38698 Cancer/an
16	1155	30.5	479	8 ADU9231	ADU9231 AAC2-2 tu
17	1151.5	29.9	480	6 AAC16438	Aac16438 Human nuc
18	1135.5	29.9	480	7 ABU64322	ABU64322 AAC2-1 pr
19	1135.5	29.9	480	8 ADU92228	ADU92228 AAC2-1 tu
20	1122.5	29.6	518	4 AAE11887	AAE11887 Angiogene
21	912.5	24.1	362	9 AEA20968	AEa20968 Novel hum
22	678.5	17.9	667	8 ADP2538	ADp2538 Sea-squir
23	658	17.3	129	9 AEB10947	Aeb10947 Human BCL
24	658	17.3	129	9 AEB10971	Aeb10971 Human BTB

25	618.5	16.3	810	3 AAY73351	Aay73351 HTRM clon
26	610	16.1	803	7 ADD45510	Add45510 Human Pro
27	610	16.1	803	8 ADG30638	Adg30638 Human tub
28	609	16.1	803	4 AAM39272	Aam39272 Human pol
29	609	16.1	804	4 AAM41058	Aam41058 Human pol
30	602	15.9	127	9 AEB10948	Aeb10948 Human BCL
31	602	15.9	803	2 AAW81756	Aaw81756 Myc-B-indi
32	588	15.5	756	7 ADF17459	Adf17459 Mouse IL-
33	564.5	14.9	765	6 ABP96229	Abp96229 Human nuc
34	560	14.8	765	8 ADR09346	Adr09346 Human pro
35	540	14.2	688	5 ABB82513	Abb82513 Human rep
36	535	14.1	775	7 ADC31774	Adc31774 Human nov
37	522.5	13.8	603	4 AAM41821	Aam41821 Human pol
38	522.5	13.8	610	4 AAB53761	Aab53761 Human pro
39	522.5	13.8	610	4 AAB50159	Abb50159 Human tra
40	522.5	13.8	610	5 AAM47779	Aam47779 Human myo
41	522.5	13.8	610	5 AAM47790	Aam47790 Murine my
42	522	13.8	682	8 ADM90925	Adm90925 Human pha
43	518	13.7	706	9 ADY71947	Ady71947 Mouse GZF
44	517	13.6	711	5 AAC021779	Aac021779 Lung-spec
45	517	13.6	711	9 ADY71945	Ady71945 Human GZF

ALIGNMENTS

RESULT 1
ID AAY78793 standard; protein; 706 AA.
AAAY78793;

19-MAY-2000 (first entry)
Human BCL-6 protein sequence.

BCL-6; human; B-cell lymphoma; regulator; non-Hodgkin's lymphoma;
diffuse type B-cell lymphoma.

Homo sapiens.

WO200000185-A1.

06-JAN-2000.

30-JUN-1999; 99WO-US014703.

30-JUN-1998; 98US-00107058.

(UYCO) UNIV COLUMBIA NEW YORK.

Dalla-Favera R, Niu H;

WPI; 2000-160631/14.

Novel methods for regulating BCL-6 levels in cells used to treat humans with lymphoma.

Example 2; Fig 10; 159pp; English.

This sequence represents the human bcl-6 protein sequence. The invention relates to a vertebrate bcl-6 locus which is the breakpoint cluster region in B-cell lymphomas, and contains a bcl-6 gene encoding a BCL-6 polypeptide. Administration of a molecule which induces phosphorylation of BCL-6 and thereby induces BCL-6 degradation, can be used as a method of regulating BCL-6 in cells. The methods of the invention can be used to regulate, and especially to decrease BCL-6 levels in cells. The methods may also be used to screen putative therapeutic agents for treatment of non-Hodgkin's lymphoma, by contacting cells from lymphoma and normal cells with the agent, and after a period of time comparing the amount of bcl-6 nucleic acid in each sample, a difference indicating the effectiveness of the agent. The bcl-6 gene is a source of probes and primers, which are used to diagnose diffuse-type B cell lymphoma and B

CC cell lymphoma in a subject. Anti-Bcl-6 antibodies may also be used for
 CC this purpose. The methods are useful for treating non-Hodgkin's lymphoma
 XX
 SQ Sequence 706 AA;

Query Match 100.0%; Score 3793; DB 3; Length 706;
 Best Local Similarity 100.0%; Pred. No. 9.8e-284;
 Matches 706; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MASPADSCIOFTRHSDVILNINRLSRDILTDVIVYVRSREOPRAHKTVMACSGIFYSI 60
DB 1 MASPADSCIOFTRHSDVILNINRLSRDILTDVIVYVRSREOPRAHKTVMACSGIFYSI 60
QY 61 FTDOUKCNLSVINLDEINBEGCILLDMFTSRLNLRGNNIMAWATAMYLQMEHVDT 120
DB 61 FTDOUKCNLSVINLDEINBEGCILLDMFTSRLNLRGNNIMAWATAMYLQMEHVDT 120
QY 121 CRKFTKASAEWVSAIKPPREFLNSRMLMPDIMA YRGREVENNLPLRSAPGCSRFAF 180
DB 121 CRKFTKASAEWVSAIKPPREFLNSRMLMPDIMA YRGREVENNLPLRSAPGCSRFAF 180
QY 181 APSLYSGLSTPPASYSMSYSHLPVSSILFSDEEFDVDMVAMPFKERALLPCDSAPVPVG 240
DB 181 APSLYSGLSTPPASYSMSYSHLPVSSILFSDEEFDVDMVAMPFKERALLPCDSAPVPVG 240
QY 241 EYSRPTLEVPNVCHSNITSPKETTPEEARSMDHVSVAAGLKPAAASANAPFPDCKAS 300
DB 241 EYSRPTLEVPNVCHSNITSPKETTPEEARSMDHVSVAAGLKPAAASANAPFPDCKAS 300
QY 301 KEERPSSEDEIALHSEPPNAPLNKRGIVSPQSKDCQPNSPTEACSSKNACILQASG 360
DB 301 KEERPSSEDEIALHSEPPNAPLNKRGIVSPQSKDCQPNSPTEACSSKNACILQASG 360
QY 361 SEPAPKPTDPKACNMKKYKFTVINSINONAKKPGQAEIGRLSPRAYTAPACOPMPMP 420
DB 361 SEPAPKPTDPKACNMKKYKFTVINSINONAKKPGQAEIGRLSPRAYTAPACOPMPMP 420
QY 421 ENMDLOSPTKLASGSDSTTPQASRLNINVTNSMTSPSSSSSHSPLYMHPPKTCSS 480
DB 421 ENMDLOSPTKLASGSDSTTPQASRLNINVTNSMTSPSSSSSHSPLYMHPPKTCSS 480
QY 481 OSPQHAEMCLHTGPTFAEEMGETOSEYSDSCENGAFCNECDCAFSEASLKRHTLT 540
DB 481 OSPQHAEMCLHTGPTFAEEMGETOSEYSDSCENGAFCNECDCAFSEASLKRHTLT 540
QY 541 HSDKPYKCDRCQASFFYKGNLASHKTVHGEKPYRCNICGAQFNRPANLKTHTRIHSGEK 600
DB 541 HSDKPYKCDRCQASFFYKGNLASHKTVHGEKPYRCNICGAQFNRPANLKTHTRIHSGEK 600
QY 601 PYKCEFCGARFVQVAHLRAHVLHTHGEKPYPCICCTRRRHLOTLKSHLRHTHGEKPYHC 660
DB 601 PYKCEFCGARFVQVAHLRAHVLHTHGEKPYPCICCTRRRHLOTLKSHLRHTHGEKPYHC 660
QY 661 EKCNLHFRHKSQRLRLRQHGAIITNTKVOYRSATDLPPELPKAC 706
DB 661 EKCNLHFRHKSQRLRLRQHGAIITNTKVOYRSATDLPPELPKAC 706

RESULT 2
AAB29640
ID AAB29640 standard; protein; 706 AA.
AC AAB29640;
DT 23-FEB-2001 (first entry)
XX
DE Human bcl-6 transcriptional repressor.
XX Human; bcl-6; transcriptional repressor; germinal centre formation;
XX Th-2 mediated antibody affinity maturation; apoptosis regulator;
XX chromosome 3q27; lymphoma; acute lymphoblastic leukaemia;
XX post-transplant lymphoproliferative disorder; expression inhibition;
XX antisense therapy.

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XX Homo sapiens.
OS US6140125-A.
XX 31-OCT-2000.
XX 15-OCT-1999; 99US-00418640.
XX 15-OCT-1999; 99US-00418640.
XX (ISIS-) ISIS PHARM INC.
XX Taylor JK, Cowseart LM;
XX WPI; 2001-048959/06.
XX N-PSDB; AAC81137.
XX Antisense compounds which specifically hybridize with and inhibit human
XX bcl-6 expression, useful for treating bcl-6 related disorders, and
XX preventing or delaying inflammation or tumor formation.
XX Disclosure; Col 47-52; 42pp; English.
XX
XX This sequence represents human bcl-6. Bcl-6 (also known as B-cell
XX CLL/lymphoma 6, zinc finger protein 51 and LA23) is a sequence-specific
XX DNA-binding transcriptional repressor. The bcl-6 gene is expressed in
XX germinal centre B- and T-cells and is required for germinal centre
XX formation and Th-2 mediated antibody affinity maturation. Bcl-6 may also
XX play a role in the regulation of apoptosis. The bcl-6 gene is located on
XX chromosome 3q27, a region which undergoes a high frequency of
XX translocation events. Such chromosomal translocations can result in
XX aberrant forms of bcl-6, which are strongly implicated in the
XX pathogenesis of several types of lymphoma, and have also been reported in
XX acute lymphoblastic leukaemia and post-transplant lymphoproliferative
XX disorders. The invention relates to antisense oligonucleotides targeted
XX to the human bcl-6 gene, which inhibit its expression. A series of
XX oligonucleotides (AAC81144-C81223) were designed to target different
XX regions of the human bcl-6 mRNA, and were analysed for their effect on
XX bcl-6 mRNA levels by quantitative real-time PCR. The oligonucleotides of
XX the invention are useful for diagnosis, prevention and treatment of
XX conditions associated with aberrant forms of bcl-6, such as lymphomas,
XX acute lymphoblastic leukaemia and post-transplant lymphoproliferative
XX disorders
XX
XX Sequence 706 AA:
SQ
Query Match 100.0%; Score 3793; DB 4; Length 706;
Best Local Similarity 100.0%; Pred. No. 9.8e-284;
Matches 706; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASPADSCIOFTRHSDVILNINRLSRDILTDVIVYVRSREOPRAHKTVMACSGIFYSI 60
DB 1 MASPADSCIOFTRHSDVILNINRLSRDILTDVIVYVRSREOPRAHKTVMACSGIFYSI 60
QY 61 FTDOUKCNLSVINLDEINBEGCILLDMFTSRLNLRGNNIMAWATAMYLQMEHVDT 120
DB 61 FTDOUKCNLSVINLDEINBEGCILLDMFTSRLNLRGNNIMAWATAMYLQMEHVDT 120
QY 121 CRKFTKASAEWVSAIKPPREFLNSRMLMPDIMA YRGREVENNLPLRSAPGCSRFAF 180
DB 121 CRKFTKASAEWVSAIKPPREFLNSRMLMPDIMA YRGREVENNLPLRSAPGCSRFAF 180
QY 181 APSLYSGLSTPPASYSMSYSHLPVSSILFSDEEFDVDMVAMPFKERALLPCDSAPVPVG 240
DB 181 APSLYSGLSTPPASYSMSYSHLPVSSILFSDEEFDVDMVAMPFKERALLPCDSAPVPVG 240
QY 241 EYSRPTLEVPNVCHSNITSPKETTPEEARSMDHVSVAAGLKPAAASANAPFPDCKAS 300
DB 241 EYSRPTLEVPNVCHSNITSPKETTPEEARSMDHVSVAAGLKPAAASANAPFPDCKAS 300
QY 301 KEERPSSEDEIALHSEPPNAPLNKRGIVSPQSKDCQPNSPTEACSSKNACILQASG 360
DB 301 KEERPSSEDEIALHSEPPNAPLNKRGIVSPQSKDCQPNSPTEACSSKNACILQASG 360

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Db 301 KEEBRSSEDEIALHFEPPNAPLNKGLVSPQSDQCPNSPTACSSKACILQASG 360
 Qy 361 SPKASPTDPKACNMKKYKFIIVNSLNQNAKPGQEGAEIGRLSPRAYTAPPAQPMER 420
 Db 361 SPKASPTDPKACNMKKYKFIIVNSLNQNAKPGQEGAEIGRLSPRAYTAPPAQPMER 420
 Qy 421 ENIDLOSPYTLASAGEDSTIPQASRLNNIYVRSWTGSPRSSSESHSLYMHPPCTSCGS 480
 Db 421 ENIDLOSPYTLASAGEDSTIPQASRLNNIYVRSWTGSPRSSSESHSLYMHPPCTSCGS 480
 Qy 481 QSPQHAEMCHTAGPTFAEEMGETQSEYSDSSCENGAFCNECDCRSESEASLKRHTLOT 540
 Db 481 QSPQHAEMCHTAGPTFAEEMGETQSEYSDSSCENGAFCNECDCRSESEASLKRHTLOT 540
 Qy 541 HSDKPYKCDRCQASFRYKGNLASHKVTHTGKPYPCNICGAQFNRPANLKTHTRIHSGEK 600
 Db 541 HSDKPYKCDRCQASFRYKGNLASHKVTHTGKPYPCNICGAQFNRPANLKTHTRIHSGEK 600
 Qy 601 PYKCTCGARFVQVAHLRAHVLHTGKPYPCNICGTRFRHLQTLKSHLRHTGKPYHC 660
 Db 601 PYKCTCGARFVQVAHLRAHVLHTGKPYPCNICGTRFRHLQTLKSHLRHTGKPYHC 660
 Qy 661 EKCNIHFRHKSQRLHLRQKHGALTNTKQYRVASATDLPPELPKAC 706
 Db 661 EKCNIHFRHKSQRLHLRQKHGALTNTKQYRVASATDLPPELPKAC 706

RESULT 3

ADL82847
 ID ADL82847 standard; protein; 706 AA.

AC ADL82847;

DT 17-JUN-2004 (first entry)

DE Human PRO26296, SEQ ID 49.

XX Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;
 KW Antiallergic; Muscular; Neuroprotective; Nephrotoxic; Antiinflammatory;
 KM Gene Therapy; P50; B cell related disorder; cancer;
 KM Immune-mediated inflammatory disease; human.

XX Homo sapiens.

XX WO2004024097-A2.

XX 25-MAR-2004.

XX 15-SEP-2003; 2003WO-US029097.

XX 16-SEP-2002; 2002US-0411392P.

XX (GETH) GENENTECH INC.

XX Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI,
 PI Wu TD;

XX WPI: 2004-329389/30.

XX N-PSDB; ADL82846.

XX New PRO polypeptide, useful for diagnosing and treating a B cell related
 PT disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune
 PT mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.

XX Claim 10; Fig 49; 695bp; English.

XX The present invention relates to PRO proteins and their coding sequences.
 CC The PRO proteins are useful for diagnosing and treating a B cell related
 CC disorder, e.g. X-linked infantile hypogammaglobulinemia, polyasaccharide
 CC antigen unresponsiveness, selective IGA deficiency, selective IGM
 CC deficiency, selective deficiency of IgG subclasses, immunodeficiency with
 CC hyper IGM, transient hypogammaglobulinemia of infancy, Burkitt's
 CC lymphoma, intermediate lymphoma, follicular lymphoma, type II

CC hypersensitivity, rheumatoid arthritis, autoimmune mediated haemolytic
 CC anemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or
 CC ankylosing spondylitis. The PRO proteins are also useful for preparing a
 CC medicament for treating a condition that is responsive to the PRO
 CC protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO
 CC coding sequences are useful as hybridization probes in chromosome and
 CC gene mapping, in preparing PRO proteins, or in generating transgenic
 CC animals or knockout animals, which in turn are useful in the development
 CC and screening of therapeutically useful reagents.

XX Sequence 706 AA:

Query Match 100.0%; Score 3793; DB 8; Length 706;

Best Local Similarity 100.0%; Pred No. 9.8e-284;

Matches 706; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASPADSCIOFTTHASDVLNLRSRDILTDVIVSRQFRANKTVLMACGIFYSI 60

Db 1 MASPADSCIOFTTHASDVLNLRSRDILTDVIVSRQFRANKTVLMACGIFYSI 60

Qy 61 FTDQLKCNLSVINLDEINPEGFCILLDFYTRNLNREGNIMAVATAMYLQMEHVVD 120

Db 61 FTDQLKCNLSVINLDEINPEGFCILLDFYTRNLNREGNIMAVATAMYLQMEHVVD 120

Qy 121 CRKPIKASBAEMVSAIKPREEFPLNSRMLPQDIMA YRGREVENNLPISAPGCEBRAF 180

Db 121 CRKPIKASBAEMVSAIKPREEFPLNSRMLPQDIMA YRGREVENNLPISAPGCEBRAF 180

Qy 181 APSLYSGISTPPASYSNYSHPVSSLLFSDERFDVMPVAPNPPKERALPCDSARVPV 240

Db 181 APSLYSGISTPPASYSNYSHPVSSLLFSDERFDVMPVAPNPPKERALPCDSARVPV 240

Qy 241 EYSRPTLEVPNVCHSNITSPKETTIPPEARSDMNYVAGLKPAAPSARAPYPCCKAS 300

Db 241 EYSRPTLEVPNVCHSNITSPKETTIPPEARSDMNYVAGLKPAAPSARAPYPCCKAS 300

Qy 301 KEEBRSSEDEIALHFEPPNAPLNKGLVSPQSDQCPNSPTACSSKACILQASG 360

Db 301 KEEBRSSEDEIALHFEPPNAPLNKGLVSPQSDQCPNSPTACSSKACILQASG 360

Qy 361 SPKASPTDPKACNMKKYKFIIVNSLNQNAKPGQEGAEIGRLSPRAYTAPPAQPMER 420

Db 361 SPKASPTDPKACNMKKYKFIIVNSLNQNAKPGQEGAEIGRLSPRAYTAPPAQPMER 420

Qy 421 ENIDLOSPYTLASAGEDSTIPQASRLNNIYVRSWTGSPRSSSESHSLYMHPPCTSCGS 480

Db 421 ENIDLOSPYTLASAGEDSTIPQASRLNNIYVRSWTGSPRSSSESHSLYMHPPCTSCGS 480

Qy 481 QSPQHAEMCHTAGPTFAEEMGETQSEYSDSSCENGAFCNECDCRSESEASLKRHTLOT 540

Db 481 QSPQHAEMCHTAGPTFAEEMGETQSEYSDSSCENGAFCNECDCRSESEASLKRHTLOT 540

Qy 541 HSDKPYKCDRCQASFRYKGNLASHKVTHTGKPYPCNICGAQFNRPANLKTHTRIHSGEK 600

Db 541 HSDKPYKCDRCQASFRYKGNLASHKVTHTGKPYPCNICGAQFNRPANLKTHTRIHSGEK 600

Qy 601 PYKCTCGARFVQVAHLRAHVLHTGKPYPCNICGTRFRHLQTLKSHLRHTGKPYHC 660

Db 601 PYKCTCGARFVQVAHLRAHVLHTGKPYPCNICGTRFRHLQTLKSHLRHTGKPYHC 660

Qy 661 EKCNIHFRHKSQRLHLRQKHGALTNTKQYRVASATDLPPELPKAC 706

Db 661 EKCNIHFRHKSQRLHLRQKHGALTNTKQYRVASATDLPPELPKAC 706

RESULT 4

ADL14017
 ID ADL14017 standard; protein; 706 AA.

AC ADL14017;

DT 21-OCT-2004 (first entry)

DE Human NF-kappaB pathway-associated protein SeqID18.
 XX NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;
 XX antiarthritic; antineumatic; gastrointestinal-gen; antiaesthetic;
 XX antileukosclerotic; immunomodulator; cerebroprotective; vasotropic;
 XX immunosuppressive; vulnary; gene therapy; immune disorder;
 XX inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;
 XX hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;
 XX hyper-igm syndrome; hypodidrotic ectodermal dysplasia;
 XX X-linked anhidrotic ectodermal dysplasia; immunodeficiency;
 XX viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV, influenza;
 XX viral replication; host cell survival; evasion of immune response;
 XX rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;
 XX atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;
 XX autoimmune disorder; hyper immune activity;
 XX aberrant acute phase response; hypercongenital condition; birth defect;
 XX necrotic lesion; wound; organ transplant rejection;
 XX aberrant signal transduction; proliferating disorder; cancer;
 XX HIV propagation; human.
 XX Homo sapiens.
 OS
 PN WO2004065577-A2.
 XX
 PD 05-AUG-2004.
 XX
 PF 13-JUN-2004, 2004MO-US000798.
 XX
 PR 14-JAN-2003, 2003US-0440068P.
 XX
 PR 12-MAY-2003, 2003US-0469757P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Nadler SG, Neubauer MG, Feder JN, Carman J,
 DR MPI; 2004-562168/54.
 XX
 DR N-PDB; ADR14016.
 XX
 XX New isolated polynucleotides and polypeptides associated with NF-kappaB
 PT pathway, useful for diagnosing, treating, or preventing disorders or
 PT diseases associated with NF-kappaB pathway.
 XX
 PS Claim 6; SEQ ID NO 18; 237pp; English.
 XX
 CC This invention relates to the novel association of protein sequences (and
 CC the genes which encode them) to the NF-kappaB pathway. The invention may
 CC be useful for the production of compounds with an antiinflammatory,
 CC cytostatic, hepatotropic, virucide, antiaesthetic, antineumatic,
 CC gastrointestinal-gen, antiaesthetic, antileukosclerotic,
 CC immunomodulator, cerebroprotective, vasotropic, immunosuppressive or
 CC vulnary activity or for gene therapy. The proteins and nucleotides are
 CC useful for diagnosing, preventing, treating, or ameliorating conditions
 CC or diseases associated with the NF-kappaB pathway. The condition is an
 CC immune disorder, an inflammatory disorder, an inflammatory disorder
 CC related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,
 CC hepatic disorders, Hodgkin's lymphoma, haematopoietic tumours, hyper-igm
 CC syndrome, hypodidrotic ectodermal dysplasia, X-linked anhidrotic
 CC ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,
 CC hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell
 CC survival, evasion of immune responses, rheumatoid arthritis, inflammatory
 CC bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick
 CC syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper
 CC immune activity, disorders related to aberrant acute phase responses,
 CC hypercongenital conditions, birth defects, necrotic lesions, wounds,
 CC organ transplant rejection, conditions related to organ transplant
 CC rejection, disorders related to aberrant signal transduction,
 CC proliferating disorders, cancers and HIV propagation in cells infected
 CC with other viruses. The present sequence is that of a human protein which
 CC is subject to the novel association with the NF-kappaB pathway of the
 CC invention. Note: This sequence does not appear in the specification but
 CC was obtained by the indexer from Genbank.
 XX
 XX Sequence 706 AA.

Query Match 100.0%; Score 3793; DB 8; Length 706;
 Best Local Similarity 100.0%; Pred. No. 9.8e-284;
 Matches 706; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASPDSCIOPTFRASDVILNLRSRDILDDVIVVSRQOPRAKTVMAQGLFYSI 60
 DB 1 MASPDSCIOPTFRASDVILNLRSRDILDDVIVVSRQOPRAKTVMAQGLFYSI 60
 QY 61 FTDQKCNLSVINLDPETINPBGFCILDPMTYSLNLRBGNIMVMTMTYOMEHVDT 120
 DB 61 FTDQKCNLSVINLDPETINPBGFCILDPMTYSLNLRBGNIMVMTMTYOMEHVDT 120
 QY 61 FTDQKCNLSVINLDPETINPBGFCILDPMTYSLNLRBGNIMVMTMTYOMEHVDT 120
 DB 61 FTDQKCNLSVINLDPETINPBGFCILDPMTYSLNLRBGNIMVMTMTYOMEHVDT 120
 QY 121 CKKFKTASAEVNSAIKPPREFFLNSRMIPDDIMAYGREYVENNPLRSAPGESRAF 180
 DB 121 CKKFKTASAEVNSAIKPPREFFLNSRMIPDDIMAYGREYVENNPLRSAPGESRAF 180
 QY 121 CKKFKTASAEVNSAIKPPREFFLNSRMIPDDIMAYGREYVENNPLRSAPGESRAF 180
 DB 121 CKKFKTASAEVNSAIKPPREFFLNSRMIPDDIMAYGREYVENNPLRSAPGESRAF 180
 QY 181 APSLYSGLSTPPASYSMTSHLPVSSILPSDEEFDVRMPVNPFPKERALPCDSARPVG 240
 DB 181 APSLYSGLSTPPASYSMTSHLPVSSILPSDEEFDVRMPVNPFPKERALPCDSARPVG 240
 QY 181 APSLYSGLSTPPASYSMTSHLPVSSILPSDEEFDVRMPVNPFPKERALPCDSARPVG 240
 DB 181 APSLYSGLSTPPASYSMTSHLPVSSILPSDEEFDVRMPVNPFPKERALPCDSARPVG 240
 QY 241 EYSRPTLEVSINVCHSNITSPKETTPEBARSDMHSVAGLKPAAAPARNAPYPCDKAS 300
 DB 241 EYSRPTLEVSINVCHSNITSPKETTPEBARSDMHSVAGLKPAAAPARNAPYPCDKAS 300
 QY 241 EYSRPTLEVSINVCHSNITSPKETTPEBARSDMHSVAGLKPAAAPARNAPYPCDKAS 300
 DB 241 EYSRPTLEVSINVCHSNITSPKETTPEBARSDMHSVAGLKPAAAPARNAPYPCDKAS 300
 QY 301 KEERPPSSDELTALPEPPNAPLNKGLVSPQSPKSDCQPSPTBACSSKACILQASG 360
 DB 301 KEERPPSSDELTALPEPPNAPLNKGLVSPQSPKSDCQPSPTBACSSKACILQASG 360
 QY 301 KEERPPSSDELTALPEPPNAPLNKGLVSPQSPKSDCQPSPTBACSSKACILQASG 360
 DB 301 KEERPPSSDELTALPEPPNAPLNKGLVSPQSPKSDCQPSPTBACSSKACILQASG 360
 QY 361 SPPAKSPDTPKACNNKKYFIVLNSLNQAKGQGEQALGLSPRAYTAPACQPMMP 420
 DB 361 SPPAKSPDTPKACNNKKYFIVLNSLNQAKGQGEQALGLSPRAYTAPACQPMMP 420
 QY 361 SPPAKSPDTPKACNNKKYFIVLNSLNQAKGQGEQALGLSPRAYTAPACQPMMP 420
 DB 361 SPPAKSPDTPKACNNKKYFIVLNSLNQAKGQGEQALGLSPRAYTAPACQPMMP 420
 QY 421 ENLIDQSPYKLSASGEDSTIPQASRLNITVNSMTGSPSSSSSPLYMHPKCTSCS 480
 DB 421 ENLIDQSPYKLSASGEDSTIPQASRLNITVNSMTGSPSSSSSPLYMHPKCTSCS 480
 QY 421 ENLIDQSPYKLSASGEDSTIPQASRLNITVNSMTGSPSSSSSPLYMHPKCTSCS 480
 DB 421 ENLIDQSPYKLSASGEDSTIPQASRLNITVNSMTGSPSSSSSPLYMHPKCTSCS 480
 QY 481 OSPOHAEWCLTAGPTFAEMGETOSEYSDSCENGAFPCNCDPFSSEASIKHTTLOT 540
 DB 481 OSPOHAEWCLTAGPTFAEMGETOSEYSDSCENGAFPCNCDPFSSEASIKHTTLOT 540
 QY 481 OSPOHAEWCLTAGPTFAEMGETOSEYSDSCENGAFPCNCDPFSSEASIKHTTLOT 540
 DB 481 OSPOHAEWCLTAGPTFAEMGETOSEYSDSCENGAFPCNCDPFSSEASIKHTTLOT 540
 QY 541 HSDKPYKCDRCQASFRYKGNLASHKTVHTGKPYRCNCGAOPNRPANLKTHTRIHSGEK 600
 DB 541 HSDKPYKCDRCQASFRYKGNLASHKTVHTGKPYRCNCGAOPNRPANLKTHTRIHSGEK 600
 QY 541 HSDKPYKCDRCQASFRYKGNLASHKTVHTGKPYRCNCGAOPNRPANLKTHTRIHSGEK 600
 DB 541 HSDKPYKCDRCQASFRYKGNLASHKTVHTGKPYRCNCGAOPNRPANLKTHTRIHSGEK 600
 QY 601 PYKCTCGARFYQVAHLRAHVLITGKPYPCICGTRFRHLQTLKSHIRHTGKPYHC 660
 DB 601 PYKCTCGARFYQVAHLRAHVLITGKPYPCICGTRFRHLQTLKSHIRHTGKPYHC 660
 QY 601 PYKCTCGARFYQVAHLRAHVLITGKPYPCICGTRFRHLQTLKSHIRHTGKPYHC 660
 DB 601 PYKCTCGARFYQVAHLRAHVLITGKPYPCICGTRFRHLQTLKSHIRHTGKPYHC 660
 QY 661 EKCNIHFRHKSQRLRLRKHGALITNTKYQVVSATDLPPELPCAK 706
 DB 661 EKCNIHFRHKSQRLRLRKHGALITNTKYQVVSATDLPPELPCAK 706
 QY 661 EKCNIHFRHKSQRLRLRKHGALITNTKYQVVSATDLPPELPCAK 706
 DB 661 EKCNIHFRHKSQRLRLRKHGALITNTKYQVVSATDLPPELPCAK 706

RESULT 5
 ID ADY19590 standard; protein; 706 AA.
 XX
 XX ADY19590;
 AC
 XX
 XX 05-MAY-2005 (first entry)
 DT
 XX
 DE PRO polypeptide SEQ ID NO 5396.
 XX
 XX Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;
 XX Antineumatic; Antiarthritic; Osteopathic; Hemoclastic; Antiaesthetic;
 XX Antileukosclerotic; Nephrotropic; CNS-Gen.; Hepatotropic;
 XX virucide; Gastrointestinal-Gen.; Antiposrotatic; Antiaesthetic;
 XX Antiallergic; diagnosis.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO2005016962-A2.

XX 24-FEB-2005.
XX 11-AUG-2004; 2004MO-US026249.
XX 11-AUG-2003; 2003US-0493546P.
XX (GEM) GENENTECH INC.
XX Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;
XX WPI; 2005-182330/19.
XX
XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and
XX treating an immune related disorder, e.g. systemic lupus erythematosus,
XX rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.
XX
XX Claim 8; SEQ ID NO 5396; 158bp; English.
XX
XX The invention relates to an isolated nucleic acid encoding a PRO
XX polypeptide. The polypeptide, agonist or an antagonist, antibody,
XX composition, and method are useful for diagnosing and treating an immune
XX related disorder, e.g. systemic lupus erythematosus, rheumatoid
XX arthritis. The present sequence represents a PRO polypeptide.
XX
XX Sequence 706 AA;
XX

Query Match 100.0%; Score 3793; DB 9; Length 706;
Best Local Similarity 100.0%; Pred. No. 9.8e-284;
Matches 706; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASPADSCIOFTRHASDVLTNLTNRSDILTDVIVVSREOPRAKTVLMACSGLFYSI 60
DB 1 MASPADSCIOFTRHASDVLTNLTNRSDILTDVIVVSREOPRAKTVLMACSGLFYSI 60
QY 61 FTDLKCNLYINADPEINPBGFCILDFMTSTLNAREGINAVMATAMLOMEHYVDT 120
DB 61 FTDLKCNLYINADPEINPBGFCILDFMTSTLNAREGINAVMATAMLOMEHYVDT 120
QY 121 CRKTKASAEAMVAIKPREEFLNSRLMPQDIMAARGVENVNLLPLRSGPCESRAF 180
DB 121 CRKTKASAEAMVAIKPREEFLNSRLMPQDIMAARGVENVNLLPLRSGPCESRAF 180
QY 181 APSLYSGSTPPASYSMTSHLPVSSLLFSDEFRDVNPVNPPEKRALPCDSARPYVG 240
DB 181 APSLYSGSTPPASYSMTSHLPVSSLLFSDEFRDVNPVNPPEKRALPCDSARPYVG 240
QY 241 EYSRPTLEVSBNVCHSNISPKETIPERASDMETYSVAGLKPAPASARNAPYPCDKAS 300
DB 241 EYSRPTLEVSBNVCHSNISPKETIPERASDMETYSVAGLKPAPASARNAPYPCDKAS 300
QY 301 KEERPPSEDEITAHFEPPNAPLNKGLVSPQSPKSCQNSPTEACSSNACTLOASG 360
DB 301 KEERPPSEDEITAHFEPPNAPLNKGLVSPQSPKSCQNSPTEACSSNACTLOASG 360
QY 361 SPPAKSPDPKACMKKTKFTVINSINQNAKPGEGEOLRLSPRAYTAPACOPPEP 420
DB 361 SPPAKSPDPKACMKKTKFTVINSINQNAKPGEGEOLRLSPRAYTAPACOPPEP 420
QY 421 ENLDIQSFTKLSASGEDSTIPQASHLNINVRSMTSGSRSSSESHSLYMHPPKCTSCGS 480
DB 421 ENLDIQSFTKLSASGEDSTIPQASHLNINVRSMTSGSRSSSESHSLYMHPPKCTSCGS 480
QY 481 OSPHAEWCHTAGTFAEMGEOTSEYSDSCENGAFFCNECDRESEBSLKHHTLOT 540
DB 481 OSPHAEWCHTAGTFAEMGEOTSEYSDSCENGAFFCNECDRESEBSLKHHTLOT 540
QY 541 HSDKPYKCDRCQASFRYKGNLASHKTVTGEKPYRCNIGQAFNRPANLKTHTRIHSEK 600
DB 541 HSDKPYKCDRCQASFRYKGNLASHKTVTGEKPYRCNIGQAFNRPANLKTHTRIHSEK 600
QY 601 PYKCTGARFVQVAHLRAHVLITGGEKPYCEICGTFRHLQTLKSHLRIHTEKPYHC 660
DB 601 PYKCTGARFVQVAHLRAHVLITGGEKPYCEICGTFRHLQTLKSHLRIHTEKPYHC 660

DB 601 PYKCTGARFVQVAHLRAHVLITGGEKPYCEICGTFRHLQTLKSHLRIHTEKPYHC 660
QY 661 EKNLHFRKKSQURLRLRQKGAITTTKVOYVSATDLPPELPKAC 706
DB 661 EKNLHFRKKSQURLRLRQKGAITTTKVOYVSATDLPPELPKAC 706
RESULT 6
ADRI4065
ID ADRI4065 standard; protein; 706 AA.
XX
XX ADRI4065;
XX
XX 21-OCT-2004 (first entry)
XX
XX Human NF-kappaB pathway-associated protein SeqId6.
XX
XX NF-kappaB pathway; antiinflammatory; cytosolic; hepatotropic; virucide;
XX antiarthritic; antirheumatic; gastrointestinal-Gen; antiaesthetic;
XX antiarteriosclerotic; immunomodulator; cerebroprotective; vasotrophic;
XX immunosuppressive; vulnery; gene therapy; immune disorder;
XX inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;
XX hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;
XX hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;
XX X-linked androgenic ectodermal dysplasia; immunodeficiency;
XX viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;
XX viral replication; host cell survival; evasion of immune response;
XX rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;
XX atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;
XX autoimmune disorder; hyper immune activity;
XX aberrant acute phase response; hypercongenital condition; birth defect;
XX necrotic lesion; wound; organ transplant rejection;
XX aberrant signal transduction; proliferating disorder; cancer;
XX HIV propagation; human.
XX
XX Homo sapiens.
XX
XX W02004065577-A2.
XX
XX 05-AUG-2004.
XX
XX 13-JAN-2004; 2004MO-US000798.
XX
XX 14-JAN-2003; 2003US-0440068P.
XX 12-MAY-2003; 2003US-0469757P.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
XX Nadler SG, Neubauer MG, Feder JN, Carman J;
XX WPI; 2004-562168/54.
XX
XX N-PSDB; ADRI4064.
XX
XX New isolated polynucleotides and polypeptides associated with NF-kappaB
XX pathway, useful for diagnosing, treating, or preventing disorders or
XX diseases associated with NF-kappaB pathway.
XX
XX Claim 6; SEQ ID NO 66; 237bp; English.
XX
XX This invention relates to the novel association of protein sequences (and
XX the genes which encode them) to the NF-kappaB pathway. The invention may
XX be useful for the production of compounds with an antiinflammatory,
XX cytosolic, hepatotropic, virucide, antiaesthetic, antirheumatic,
XX gastrointestinal-Gen, antiaesthetic, antiarteriosclerotic,
XX immunomodulator, cerebroprotective, vasotrophic, immunosuppressive or
XX vulnery activity or for gene therapy. The proteins and nucleotides are
XX useful for diagnosing, preventing, treating, or ameliorating conditions
XX or diseases associated with the NF-kappaB pathway. The condition is an
XX immune disorder, an inflammatory disorder, cancer, aberrant apoptosis,
XX related to aberrant NF-kappaB regulation, cancer, haematopoietic tumours, hyper-IgM
XX syndrome, hypohidrotic ectodermal dysplasia, X-linked androgenic
XX ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,

CC hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell
 CC survival, evasion of immune responses, rheumatoid arthritis, inflammatory
 CC bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick
 CC syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper
 CC immune activity, disorders related to aberrant acute phase responses,
 CC hyecongenital conditions, birth defects, necrotic lesions, wounds,
 CC organ transplant rejection, conditions related to organ transplant
 CC rejection, disorders related to aberrant signal transduction,
 CC proliferating disorders, cancers and HIV propagation in cells infected
 CC with other viruses. The present sequence is that of a human protein which
 CC is subject to the novel association with the NF-kappaB pathway of the
 CC invention. Note: This sequence does not appear in the specification but
 CC was obtained by the indexer from Genbank.

XX Sequence 706 AA:

Query Match 99.6%; Score 3777; DB 8; Length 706;
 Best Local Similarity 99.6%; Pred. No. 1.7e-282;
 Matches 703; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MASPADSCIOFTRHAGDVLLNLRSLRDILTDVIVVSRQFRAHKTVMACSGLFYSI 60
 DB 1 MASPADSCIOFTRHAGDVLLNLRSLRDILTDVIVVSRQFRAHKTVMACSGLFYSI 60
 QY 61 FTDQKCNLSVINLDEINDEGFCILLDFMYTSRLNLRGNIMAVATAMYLQMEHVDT 120
 DB 61 FTDQKCNLSVINLDEINDEGFCILLDFMYTSRLNLRGNIMAVATAMYLQMEHVDT 120
 QY 121 CRKFKASAEAWYSAIKPREEFNLNMLPQDIMAYRGVEVNNLPLRSAPGCSRA 180
 DB 121 CRKFKASAEAWYSAIKPREEFNLNMLPQDIMAYRGVEVNNLPLRSAPGCSRA 180
 QY 181 APSLYSGLSLTPPASYSYMSHLFVSSLLFSDEERDVMPVAPNPPKRALPCDSAPVRG 240
 DB 181 APSLYSGLSLTPPASYSYMSHLFVSSLLFSDEERDVMPVAPNPPKRALPCDSAPVRG 240
 QY 241 EYSRPTLEVPNVCHSNISYPKETIPBEARSDMHYSVAGLKPAAASARNAFPDCDKAS 300
 DB 241 EYSRPTLEVPNVCHSNISYPKETIPBEARSDMHYSVAGLKPAAASARNAFPDCDKAS 300
 QY 301 KEERPSSEDEIALHFEPPNAPLNKGLVSPQSPQSKDCQPNSTPTECSSKNACTIQASG 360
 DB 301 KEERPSSEDEIALHFEPPNAPLNKGLVSPQSPQSKDCQPNSTPTECSSKNACTIQASG 360
 QY 361 SPPAKSPDTPKACNMWKYKFIIVNSLNQNAKPGPEQAEIGRLSPRAYTAPPAQCPMEP 420
 DB 361 SPPAKSPDTPKACNMWKYKFIIVNSLNQNAKPGPEQAEIGRLSPRAYTAPPAQCPMEP 420
 QY 421 ENLDLQSPKLSASGEDESTIPOASRLNNINRSMWTSPPSSSHSPLVMHPPKCTSCGS 480
 DB 421 ENLDLQSPKLSASGEDESTIPOASRLNNINRSMWTSPPSSSHSPLVMHPPKCTSCGS 480
 QY 481 QSPHAEMLHTAGPTAEEMGETOSEYSDSCENGAFQCNBCDCRFSEBASLKRHTLQ 540
 DB 481 QSPHAEMLHTAGPTAEEMGETOSEYSDSCENGAFQCNBCDCRFSEBASLKRHTLQ 540
 QY 541 HSDRPYCDRCQASFRYKGNLASHKTVHTEKPYRNCICGAQFNRPANLKTTHRIHSGEK 600
 DB 541 HSDRPYCDRCQASFRYKGNLASHKTVHTEKPYRNCICGAQFNRPANLKTTHRIHSGEK 600
 QY 601 PYKCTGAPVQVAHRAHVLHTGKPPCEICGRFRHLOTLSKHLIHTGKPYHC 660
 DB 601 PYKCTGAPVQVAHRAHVLHTGKPPCEICGRFRHLOTLSKHLIHTGKPYHC 660
 QY 661 EKNLHFRHKSQRLRLRQKGAITNTKVQYRVSATDLPPELPKAC 706
 DB 661 EKNLHFRHKSQRLRLRQKGAITNTKVQYRVSATDLPPELPKAC 706

RESULT 7
 ADY15006
 ID ADY15006 standard; protein; 706 AA.

AC ADY15006;
 DT 05-MAY-2005 (first entry)
 DE PRO polypeptide SEQ ID NO 812.

XX Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;
 XX Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;
 XX Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;
 XX Virocidic; Gastrointestinal Gen.; Antipsoriatic; Antiaesthetic;
 XX Antiallergic; ds; gene; diagnosis.

OS Homo sapiens.

XX WO2005016962-A2.

XX 24-FEB-2005.

XX 11-AUG-2004; 2004WO-US026249.

XX 11-AUG-2003; 2003US-0493546F.

XX (GETH) GENENTECH INC.

XX Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;
 XX MPI, 2005-182330/19.

XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and
 XX PT treating an immune related disorder, e.g. systemic lupus erythematosus,
 XX PT rheumatoid arthritis, osteoarthritis, chyloditis, or diabetes mellitus.

XX Claim 8; SEQ ID NO 812; 158bp; English.

XX The invention relates to an isolated nucleic acid encoding a PRO
 XX polypeptide. The polypeptide, agonist or an antagonist, antibody,
 XX composition, and method are useful for diagnosing and treating an immune
 XX related disorder, e.g. systemic lupus erythematosus, rheumatoid
 XX arthritis. The present sequence represents a DNA encoding a PRO
 XX polypeptide.

XX Sequence 706 AA;

Query Match 99.6%; Score 3777; DB 9; Length 706;
 Best Local Similarity 99.6%; Pred. No. 1.7e-282;
 Matches 703; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MASPADSCIOFTRHAGDVLLNLRSLRDILTDVIVVSRQFRAHKTVMACSGLFYSI 60
 DB 1 MASPADSCIOFTRHAGDVLLNLRSLRDILTDVIVVSRQFRAHKTVMACSGLFYSI 60
 QY 61 FTDQKCNLSVINLDEINDEGFCILLDFMYTSRLNLRGNIMAVATAMYLQMEHVDT 120
 DB 61 FTDQKCNLSVINLDEINDEGFCILLDFMYTSRLNLRGNIMAVATAMYLQMEHVDT 120
 QY 121 CRKFKASAEAWYSAIKPREEFNLNMLPQDIMAYRGVEVNNLPLRSAPGCSRA 180
 DB 121 CRKFKASAEAWYSAIKPREEFNLNMLPQDIMAYRGVEVNNLPLRSAPGCSRA 180
 QY 181 APSLYSGLSLTPPASYSYMSHLFVSSLLFSDEERDVMPVAPNPPKRALPCDSAPVRG 240
 DB 181 APSLYSGLSLTPPASYSYMSHLFVSSLLFSDEERDVMPVAPNPPKRALPCDSAPVRG 240
 QY 241 EYSRPTLEVPNVCHSNISYPKETIPBEARSDMHYSVAGLKPAAASARNAFPDCDKAS 300
 DB 241 EYSRPTLEVPNVCHSNISYPKETIPBEARSDMHYSVAGLKPAAASARNAFPDCDKAS 300
 QY 301 KEERPSSEDEIALHFEPPNAPLNKGLVSPQSPQSKDCQPNSTPTECSSKNACTIQASG 360
 DB 301 KEERPSSEDEIALHFEPPNAPLNKGLVSPQSPQSKDCQPNSTPTECSSKNACTIQASG 360
 QY 361 SPPAKSPDTPKACNMWKYKFIIVNSLNQNAKPGPEQAEIGRLSPRAYTAPPAQCPMEP 420
 DB 361 SPPAKSPDTPKACNMWKYKFIIVNSLNQNAKPGPEQAEIGRLSPRAYTAPPAQCPMEP 420

DT 19-JUL-1995 (first entry)
 XX BCL-6 zinc finger protein.
 DE bcl-6 locus; non-Hodgkin lymphoma; B-cell lymphoma; B-lymphocyte;
 XX diagnostic; therapeutic; chromosome-3q27; translocation; proto-oncogene;
 KM diffuse large cell lymphoma; DLCL; zinc finger.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Region 520..541
 FT /label= Zinc-finger
 FT 548..568
 FT /label= Zinc-finger
 FT Region 576..596
 FT /label= Zinc-finger
 FT 604..624
 FT /label= Zinc-finger
 FT 632..652
 FT /label= Zinc-finger
 FT 660..681
 FT Region /label= Zinc-finger
 FT
 XX MO9429343-A1.
 XX 22-DEC-1994.
 XX 09-JUN-1994; 94MO-US006669.
 XX 09-JUN-1993; 93US-00074967.
 XX (UYCO) UNIT COLUMBIA NEW YORK.
 PA (SLOK) SLOAN KETTERING INST CANCER.
 XX
 PI Dalla-Favera R, Chaganti RS;
 DR WPI; 1995-036403/05.
 DR N-PSDB; AA068743.
 XX
 PT Nucleic acid from genetic locus bcl-6 - used to develop prods. for
 PT diagnosis and therapy of B-cell lymphoma and non-Hodgkin's lymphoma.
 PS
 XX Disclosure; Page 90-94; 129pp; English.
 XX
 XX DNA was extd. from tumor tissue of 2 cases of IgM-producing diffuse-type
 CC B-cell NHL carrying the t(3;14) (q27;q32) translocation. DNA analysis
 CC showed that the breakpoints on 3q27 were located within 3 kb of the same
 CC genomic locus, which was designated bcl-6. The human bcl-6 locus was
 CC identified by screening a phage cDNA library constructed from B1ab B-cell
 CC lymphoma mRNA. The zinc finger protein encoded by bcl-6 is given in
 CC AA068743. BCL-6 is a proto-oncogene specifically involved in the
 CC pathogenesis of diffuse large cell lymphoma. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX
 SO Sequence 706 AA:
 Query Match 99.2%; Score 3763; DB 2; Length 706;
 Best Local Similarity 99.3%; Pred. No. 2e-281;
 Matches 701; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MASPADSCIOFTTRASDVLTNLRSDILTDVTVVVSREOPRAHKTVMACSGLFYST 60
 DB 1 MASPADSCIOFTTRARVLTNLRSDILTDVTVVVSREOPRAHKTVMARGLFYST 60
 QY 61 FTDLKCNLSVINLDPINPEGFCILDPMTYSRLNREGNIMAVMATAYLQMEHYVDT 120
 DB 61 FTDLKCNLSVINLDPINPEGFCILDPMTYSRLNREGNIMAVMATAYLQMEHYVDT 120
 QY 121 CRKIKASBAEMVSAIKPRPEEFNLSRLMPDIDIMAYRGREVENNLPLASAPGCEBRAP 180
 DB 121 CRKIKASBAEMVSAIKPRPEEFNLSRLMPDIDIMAYRGREVENNLPLASAPGCEBRAP 180

QY 181 APSLYSGLSTPPASYSMTSHLPVSSLLFSDSEFRDVRMPVNPPEKRALPCDSARPYVG 240
 DB 181 APSLYSGLSTPPASYSMTSHLPVSSLLFSDSEFRDVRMPVNPPEKRALPCDSARPYVG 240
 QY 241 EYSRPTLEVSPNVCHSNITSPKETIPEBARSDMHSVAEGLKPAAPSAARNAPFPCDKAS 300
 DB 241 EYSRPTLEVSPNVCHSNITSPKETIPEBARSDMHSVAEGLKPAAPSAARNAPFPCDKAS 300
 QY 301 KEERPSSEDEIATLHFEPPNAPLNKGLVSPSPKSCOPNSPTEACSSKNACILQASG 360
 DB 301 KEERPSSEDEIATLHFEPPNAPLNKGLVSPSPKSCOPNSPTEACSSKNACILQASG 360
 QY 361 SEPAPSPDTPKACNMKKYKFIYVLSLNQNAKPGEBQAEGLSPRAYTAPACOPMWP 420
 DB 361 SEPAPSPDTPKACNMKKYKFIYVLSLNQNAKPGEBQAEGLSPRAYTAPACOPMWP 420
 QY 421 ENLDIQSPKLSASGEDSTIPQASHLNNIVNRSMTGSRSSSESHSPLYMHPKCTSCGS 480
 DB 421 ENLDIQSPKLSASGEDSTIPQASHLNNIVNRSMTGSRSSSESHSPLYMHPKCTSCGS 480
 QY 481 OSPOHAEMCIHTAGTFAEMGETOSEYSDSCENGAFPCNECDRFSSEASLKHHTLOT 540
 DB 481 OSPOHAEMCIHTAGTFAEMGETOSEYSDSCENGAFPCNECDRFSSEASLKHHTLOT 540
 QY 541 HSDKEPKCDRCQASFRYKGNLASHKTVAHTEKPYPCNIGQAQPNRPAULKTHRIHSGEK 600
 DB 541 HSDKEPKCDRCQASFRYKGNLASHKTVAHTEKPYPCNIGQAQPNRPAULKTHRIHSGEK 600
 QY 601 PYKCTCGARFVQVAHLRAVLIHTGEKYPCEICGTRFRHLQTLKSHLRIHTGEKPYHC 660
 DB 601 PYKCTCGARFVQVAHLRAVLIHTGEKYPCEICGTRFRHLQTLKSHLRIHTGEKPYHC 660
 QY 661 EKCNLHFRHKSQRLRLHROKGAITNTKYQVVSATDLPPELPKAC 706
 DB 661 EKCNLHFRHKSQRLRLHROKGAITNTKYQVVSATDLPPELPKAC 706

RESULT 10
 ID AAY78792 standard; protein; 706 AA.
 AC AAY78792;
 XX
 XX 19-MAY-2000 (first entry)
 XX
 XX Human BCL-6 protein sequence.
 XX DE
 XX Bcl-6; human; B-cell lymphoma; regulator; non-Hodgkin's lymphoma;
 KM diffuse type B-cell lymphoma.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO200000185-A1.
 PN
 XX 06-JAN-2000.
 PD
 XX 30-JUN-1999; 99WO-US014703.
 PF
 XX 30-JUN-1998; 98US-00107058.
 PR
 XX (UYCO) UNIT COLUMBIA NEW YORK.
 PA
 XX Dalla-Favera R, Niu H;
 PI
 XX WPI; 2000-160631/14.
 DR N-PSDB; AA290110.
 XX
 PT Novel methods for regulating BCL-6 levels in cells used to treat humans
 PT with lymphoma.
 XX
 XX Example; Fig 9; 159pp; English.
 XX
 CC This sequence represents the human bcl-6 protein sequence. The invention

CC relates to a vertebrate bcl-6 locus which is the breakpoint cluster
 CC region in B-cell lymphomas, and contains a bcl-6 gene encoding a BCL-6
 CC polypeptide. Administration of a molecule which induces phosphorylation
 CC of BCL-6 and thereby induces BCL-6 degradation, can be used as a method
 CC of regulating BCL-6 in cells. The methods of the invention can be used to
 CC regulate, and especially to decrease BCL-6 levels in cells. The methods
 CC may also be used to screen putative therapeutic agents for treatment of
 CC non-Hodgkin's lymphoma, by contacting cells from lymphoma and normal
 CC cells with the agent, and after a period of time comparing the amount of
 CC bcl-6 nucleic acid in each sample, a difference indicating the
 CC effectiveness of the agent. The bcl-6 gene is a source of probes and
 CC primers, which are used to diagnose diffuse-type B cell lymphoma and B
 CC cell lymphoma in a subject. Anti-BCL-6 antibodies may also be used for
 CC this purpose. The methods are useful for treating non-Hodgkin's lymphoma
 CC
 XX
 XX Sequence 706 AA;

Query Match 99.2%; Score 3763; DB 3; Length 706;
 Best Local Similarity 99.3%; Pred. No. 2e-281;
 Matches 701; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

1 MASPADSCIOFTRHNSDVLTINLRSDILTDVVIIVSREOFRAHKTVMACGGLFYSI 60
 1 MASPADSCIOFTRHNSDVLTINLRSDILTDVVIIVSREOFRAHKTVMAMGGLFYSI 60
 61 FTDLKCNLSVINLDPINDEPFCILLDPMTSLNLRBNINAMVMTATYLOMEHYVD 120
 61 FTDLKCNLSVINLDPINDEPFCILLDPMTSLNLRBNINAMVMTATYLOMEHYVD 120
 121 CRKRTKASEAMNSAIPREPEFLNSRLMPDIMAARGREVENNNPLSAPCESRAF 180
 121 CRKRTKASEAMNSAIPREPEFLNSRLMPDIMAARGREVENNNPLSAPCESRAF 180
 121 CRKRTKASEAMNSAIPREPEFLNSRLMPDIMAARGREVENNNPLSAPCESRAF 180
 181 APSYSGSLSTPPASYSMTSLPVSSLLFSDEPRDVMPPANPPKERRALPCDSARVP 240
 181 APSYSGSLSTPPASYSMTSLPVSSLLFSDEPRDVMPPANPPKERRALPCDSARVP 240
 241 EYSRPTLEVPNSVCHSNISPKETIPREARSDMHYSVAEGKPAAPSARNAVPFPCDKAS 300
 241 EYSRPTLEVPNSVCHSNISPKETIPREARSDMHYSVAEGKPAAPSARNAVPFPCDKAS 300
 301 KEERPSSEDEIALHFEPPNAPLRKGLVSPQSKDCONSSTECSSKNACILQASG 360
 301 KEERPSSEDEIALHFEPPNAPLRKGLVSPQSKDCONSSTECSSKNACILQASG 360
 361 SPPAKSTDPKACNWKYKFTVLSLNONAKRGPEOAEGLRLPRATYAPACOPMEP 420
 361 SPPAKSTDPKACNWKYKFTVLSLNONAKRGPEOAEGLRLPRATYAPACOPMEP 420
 361 SPPAKSTDPKACNWKYKFTVLSLNONAKRGPEOAEGLRLPRATYAPACOPMEP 420
 421 ENLDLQSPYTKLASGSDSTIPQASRLNNIVNRSMTGSPRSSSESHSPLYMHPKCTSCGS 480
 421 ENLDLQSPYTKLASGSDSTIPQASRLNNIVNRSMTGSPRSSSESHSPLYMHPKCTSCGS 480
 481 QSPHAEMLCHTAGPTPAEMGETQSEYSDSSCENGAFCNCCCRSESESLKXHTLOT 540
 481 QSPHAEMLCHTAGPTPAEMGETQSEYSDSSCENGAFCNCCCRSESESLKXHTLOT 540
 541 HSDKPYKCDRCQASFRKGNLASHKTYTGKPYRCNCGAOFNPAULKXHTIHSSEK 600
 541 HSDKPYKCDRCQASFRKGNLASHKTYTGKPYRCNCGAOFNPAULKXHTIHSSEK 600
 601 PYKCTGAFRVQVAHLIAHVLITGKPYRCICGTFRHLQTLKSHLRITHTGSKPYHC 660
 601 PYKCTGAFRVQVAHLIAHVLITGKPYRCICGTFRHLQTLKSHLRITHTGSKPYHC 660
 661 EKNLHFRHKSQRLRLHROKGAITNTKYQVRVSATDLPRLPRAC 706
 661 EKNLHFRHKSQRLRLHROKGAITNTKYQVRVSATDLPRLPRAC 706

XX
 AC ABB57289;
 XX
 DT 07-MAR-2002 (first entry)
 XX
 DE Mouse ischaemic condition related protein sequence SEQ ID NO:814.
 XX
 KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
 KW vasospastic ischaemia; ischaemic condition; ischaemic disease.
 XX
 OS Mus musculue.
 XX
 PN WO2001818-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 18-MAY-2001; 2001WO-JP004192.
 XX
 PR 18-MAY-2000; 2000JP-00145977.
 XX
 PA (UNIT-) UNIV NIHON SCHOOL JURIDICAL PERSON.
 XX
 PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
 XX
 DR WPI; 2002-034733/04.
 DR N-PSDB; AB199745.
 XX
 PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring
 PT expression levels of particular genes defined in the specification or by
 PT determining the expression profile of a gene group comprising these
 PT genes.
 XX
 PS Claim 2; Page 2004-2007; 2690pp; English.
 XX
 CC The present invention describes a method for examining ischaemic
 CC conditions, comprising measuring the expression levels of particular
 CC genes (I) in a test sample or determining the expression profile of a
 CC gene group in the sample comprising genes selected from (I). The method
 CC is useful for examining the ischaemic condition (e.g. compressive
 CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
 CC the expression levels of particular genes (AB199912 to AB199912, encoding the
 CC protein sequences in ABB57020 to ABB57174) or by determining the
 CC expression profile of a gene group comprising these genes. The expression
 CC levels or expression profiles produced by these genes are used as an
 CC indicator when screening for ischaemic condition-improving drugs or
 CC therapeutics for ischaemic diseases. AB199913 and AB199914 represent PCR
 CC primers for a mouse ischaemic condition related sequence, which are used
 CC in the exemplification of the present invention
 XX
 XX Sequence 707 AA;
 Query Match 95.0%; Score 3602.5; DB 5; Length 707;
 Best Local Similarity 94.2%; Pred. No. 5e-269;
 Matches 666; Conservative 14; Mismatches 26; Indels 1; Gaps 1;

1 MASPADSCIOFTRHNSDVLTINLRSDILTDVVIIVSREOFRAHKTVMACGGLFYSI 60
 1 MASPADSCIOFTRHNSDVLTINLRSDILTDVVIIVSREOFRAHKTVMACGGLFYSI 60
 61 FTDLKCNLSVINLDPINDEPFCILLDPMTSLNLRBNINAMVMTATYLOMEHYVD 120
 61 FTDLKCNLSVINLDPINDEPFCILLDPMTSLNLRBNINAMVMTATYLOMEHYVD 120
 121 CRKRTKASEAMNSAIPREPEFLNSRLMPDIMAARGREVENNNPLSAPCESRAF 180
 121 CRKRTKASEAMNSAIPREPEFLNSRLMPDIMAARGREVENNNPLSAPCESRAF 180
 181 APSYSGSLSTPPASYSMTSLPVSSLLFSDEPRDVMPPANPPKERRALPCDSARVP 239
 181 APSYSGSLSTPPASYSMTSLPVSSLLFSDEPRDVMPPANPPKERRALPCDSARVP 239
 240 GEYSRPTLEVPNSVCHSNISPKETIPREARSDMHYSVAEGKPAAPSARNAVPFPCDKA 299
 240 GEYSRPTLEVPNSVCHSNISPKETIPREARSDMHYSVAEGKPAAPSARNAVPFPCDKA 299

RESULT 11
 ABB57289
 ID ABB57289 standard; protein; 707 AA.

Db 241 NEYSRAMEVSPSLCHSNITSPKEAVPEBARSDIHVSDEGPKPAVPSANAPYFPCDXA 300
Qy 300 SKEERPSSEDEIHALHFEPPNAPLNKGLVSPQSPKSCOPSPTEACSSNACLOAS 359
Db 301 SKEERPSSEDEIHALHFEPPNAPLNKGLVSPQSPKSCOPSPTEACSSNACLOAS 360
Qy 360 GSPPAKSPDPKACNMKKYKFIYVNSLONAKPGEGEQAELRLSPRAYTAPACOPME 419
Db 361 GSPPAKSPDPKACNMKKYKFIYVNSLONAKPGEGEQAELRLSPRAYTAPACOPME 420
Qy 420 PENLDIQSPTKASAGEDSTIPQASRLNINVRSMTGSRSSSESHPLYMHPKCTSCG 479
Db 421 PAULDIOSTPKLASAGEDSTIPQASRLNINVRSLGSSRSSSESHPLYMHPKCTSCG 480
Qy 480 SOSPQAEMLHAGTTPAEEMKETSEVSDSCENGAFCPCEDCRFEESAKRHTIO 539
Db 481 SOSPQAEMLHAGTTPAEEMKETSEVSDSCENGAFCPCEDCRFEESAKRHTIO 540
Qy 540 TSHDKPYKCDRCQASFRYKGNLASHKTVHTGEKPYKNCIQAQFNPAPMLKTHRIHSGE 599
Db 541 TSHDKPYKCDRCQASFRYKGNLASHKTVHTGEKPYKNCIQAQFNPAPMLKTHRIHSGE 600
Qy 600 KPYKCTCGARFVQVAHLRAHVLHTGEKPYPCICGTFRRLQTLKSHLRHTGKPYH 659
Db 601 KPYKCTCGARFVQVAHLRAHVLHTGEKPYPCICGTFRRLQTLKSHLRHTGKPYH 660
Qy 660 CEKCNLHFRHKSQDLRLHROKGAITNTKYQVVSATDLPPELPRKAC 706
Db 661 CEKCNLHFRHKSQDLRLHROKGAITNTKYQVVSATDLPPELPRKAC 707

RESULT 12

ABM84710
ID ABM84710 standard; protein; 458 AA.

XX ABM84710;

XX DT 18-NOV-2004 (first entry)

XX DE Human diagnostic and therapeutic pprotein SEQ ID NO:4959.

XX KM gene therapy; human diagnostic and therapeutic polynucleotide; dlthp.

XX OS Homo sapiens.

XX PN WO2004023973-A2.

XX PD 25-MAR-2004.

XX PF 12-SEP-2003; 2003WO-US028227.

XX PR 12-SEP-2002; 2002US-0410259P.

XX PR 12-SEP-2002; 2002US-0410260P.

XX (INCY-) INCYTE CORP.

XX PA Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,
PI Hartshorne TA, Suchorolski MT, Altus CM, Pites SJ, Elder LV,
PI Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP,
PI Stevens EA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH,
PI Paralta CH, Anderson SB, Rious P, Shen BJ, Wu MC, Stuve LJ,
PI Lagace RE, Spito PA, Stewart EA, Wingrove J, Vilt UA, Kitton ES,
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D,
PI Patry S, Shi X, Suarez CJ,

XX WPI; 2004-329368/30.
DR N-PSDB; ACN43362.

XX PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.

PS Claim 27; Page; 190pp; English.
XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dlthp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorders, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dlthp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germ-line
CC gene therapy. The present sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/11etling.htm

XX SQ Sequence 458 AA;

Query Match 30.5%; Score 1158.5; DB 8; Length 458;
Best Local Similarity 37.6%; Pred. No. 1.5e-80;

Matches 268; Conservative 49; Mismatches 118; Indels 277; Gaps 15;

Qy 1 MASPA--DSCI-----QFTRHSDVLLNINRLSRDILTDVIVVSRQFRAHKTVMACS 54
Db 1 MGSPPAEGALGVAFETRRSHSDVGNINELRLRGLITDVTLLVGGQPLRAKAVLINGS 60
Qy 55 GLFYSLFTDQKCNLSVINLDEINPEGFCILDFMTYTRNLREGNIMAVMATMYLW 114
Db 61 GFFYSIFRGAAGVDVLSLPGPGARGFAPLIDFMTYSRLSLSPATAVAATAVYLW 120
Qy 115 EHVYDTCRKFYKASAEVNSAIKPPREFTNRMMPQIMAYRRREVNNLPLRSARG 174
Db 121 EHVQACHRFIOAS----- 134
Qy 175 CESRAFAPSLVGSLTPPASYSMYSHLPVSSLLFSDDEFRDVRMPANFPKRALPCDS 234
Db 135 -----YEPFGIS----- 141
Qy 235 ARPVGEYSRPTLEVPVCHSNITSPKETTPEARSMDHVSVAAGLKPAPDSANAPYF 294
Db 142 -----LAPL----- 145
Qy 295 PCDKASKEERPSSEDEIHALHFEPPNAPLNKGLVSPQSPKSCOPSPTEACSSNAC 354
Db 146 -----EAEPT-----PPTAP-----PPSPRRSEKHPDPTSRSS----- 176
Qy 355 ILQASGPPAKSPDPKACNMKKYKFIYVNSLONAKPGEGEQAELRLSPRAYTAPACOP 401
Db 177 ---CSGQPPSPAPDPKACNMKKYKFIYVNSLONAKPGEGEQAELRLSPRAYTAPACOP 233
Qy 402 RLSPRAYTAPACOPPEMPEENLDIOSPTKASAGEDSTIPQASRLNINVRSMTGSPRS 461
Db 234 RLSPTATVQFKGAP-----ASTPYLLTQAQDT-----SSGP----- 267
Qy 462 SESHSPLYMHPKCTSCGSGSPQAHMCLHTAGPTFAEMGTGSEYSSSCENGAFCPC 521
Db 268 SEARPL-----PGSBF-----FSQ 283
Qy 522 ECDRCSEASIKRHTLOTHSDPKYKCDRCQASFRYKGNLASHKTVHTGEKPYKNCIQA 581
Db 284 NCEAVAGSSGID-SLVPEDEKPYKQUCRSSFRYKGNLASHKTVHTGEKPYKNCIQA 342
Qy 582 OFNRPANLKTTHRIHSGEKPYKCTCGARFVQVAHLRAHVLHTGEKPYPCICGTFRFH 641
Db 343 RFRPANLKTTHRIHSGEKPYKCTCGARFVQVAHLRAHVLHTGEKPYPCICGTFRFH 402
Qy 642 LQTLKSHLRHTGKPYHCEKCNLHFRHKSQDLRLHROKGAITNTKYQVVSATDLPPEL 693
Db 403 LQTLKSHLRHTGKPYHCEKCNLHFRHKSQDLRLHROKGAITNTKYVHI 454

RESULT 13
 AB003467
 ID AB003467 standard; protein; 479 AA.
 XX
 AC AB003467;
 XX
 DT 21-JAN-2003 (first entry)
 XX
 DE Angiogenesis-associated human protein sequence #12.
 XX
 KM Human; angiogenesis-associated transcript; angiogenesis;
 KM angiogenesis-associated disease; cancer; cytostatic.
 OS Homo sapiens.
 XX
 PN WO200279492-A2.
 PD 10-OCT-2002.
 XX
 PF 14-FEB-2002; 2002WO-US004915.
 XX
 PR 14-FEB-2001; 2001US-00784356.
 PR 22-FEB-2001; 2001US-00791390.
 PR 19-APR-2001; 2001US-0285475P.
 PR 03-AUG-2001; 2001US-0310025P.
 PR 13-NOV-2001; 2001US-0350666P.
 PR 29-NOV-2001; 2001US-0334244P.
 XX
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 XX
 PI Murray R, Glynn R, Watson SR, Aziz N;
 XX
 DR WPI: 2003-040681/03.
 DR N-PSDB; ABX08750.
 PT
 PT Detecting angiogenesis-associated transcript in a cell for diagnosing and
 PT treating cancer by contacting a sample with a polynucleotide that
 PT exhibits changes in expression level as a function of time in tissue
 PT undergoing angiogenesis.
 XX
 XX Example 2; Page 190; 291pp; English.
 PS
 XX The present invention relates to methods and compositions for detecting
 CC an angiogenesis-associated transcript in a cell in a patient. The method
 CC involves contacting a biological sample from the patient with a
 CC polynucleotide that selectively hybridizes to a sequence at least 80%
 CC identical to any of the angiogenesis-associated human polynucleotide
 CC sequences given in the specification. These angiogenesis-associated
 CC polynucleotide sequences comprise genes that exhibit changes in
 CC expression levels as a function of time in tissue undergoing
 CC angiogenesis. The method and the polynucleotide sequences of the
 CC invention are useful for diagnosing and treating angiogenesis and
 CC angiogenesis-associated diseases e.g. cancer. The polynucleotide
 CC sequences are also useful in the gene therapy of such disorders. The
 CC angiogenesis-associated proteins encoded by the polynucleotide sequences
 CC are useful as a vaccine for therapeutic and prophylactic immunisation.
 CC AB003456-AB003569 represent angiogenesis-associated protein sequences
 XX
 SQ Sequence 479 AA;
 Query Match 30.5%; Score 1155; DB 6; Length 479;
 Best Local Similarity 38.3%; Pred. No. 2.9e-80;
 Matches 268; Conservative 58; Mismatches 142; Indels 232; Gaps 15;
 QY 1 MASPA--DSCI---QFTHASDVLTANLRSRDLTDVIVVSREQFRAKTYLACS 54
 DB 1 MGSPAPAGALGYVEFTRHSSDVLGNINELRLRGITLDVTLVGGQPLRAKAVLACS 60
 QY 55 GLEYSIFDOLKCNLSVINLDEINPEGFCILLDMYTSRLNREGNIMAWATAMYLQM 114
 DB 61 GFFYSIFRGAGVGVDVLSLPGGPRARGAPALIDMTYSRLKLSFATAPAVLAATYIOM 120

QY 115 EHVVDTCRKFIKASEAMVSAIKPREEFNLNMPDODIMAYRGREVENNLLPLSARG 174
 DB 121 EHVVOACHRFIQMS----- 134
 QY 175 CESRAFAFSLVSLGTPPASYSMYSHLPVSSLLPSDEEPRDVMVAPPPKRALPCDS 234
 DB 135 -----YEPILGIS----- 141
 QY 235 ARPVPGESRPTLEVPNCHSNIVSPKETIPPEARSDMHYVAEGLKPAAPSRNAPYF 294
 DB 142 -----LRPL----- 145
 QY 295 PCDKASKEERPESSBDEIALHPPNPAPLNRKGLVSPSPQKSCDQNSPTEACSSKNAC 354
 DB 146 -----EABPT-----PTAP-----PPGSRBSRGHPDPTESRS----- 176
 QY 355 ILQASGSPPAKSPPTDPAKCNMKYKFTVLNLSLQNAKPGGEQAEIGRLSPRAYTAPAC 414
 DB 177 ---CSGPPSPAPDPDPAKCNMKYKFTVLNLSLQNAKPGGEQAEIGRLSPRAYTAPAC 223
 QY 415 QPMEPEBNLDLQPTKLASGEDSTIP-QASRLNIVNRSMGTSPSSSSSHPLVNHPP 473
 DB 224 QARLPSSGDEASSSSSSSSSEBGPPIPGQSRL-----SPTATVQF----- 265
 QY 474 KCTSCGSPQAHMCLHTAGPTFAEMERGTOSEYSDSCENGAPFCNECDSPSEBASL 533
 DB 266 ---KCG--APASTPYLITSO---ADTSSPSERAPPLPGSEFFSQNCEAVAAGSSGL 316
 QY 534 KRATLQTHSDKPYKCDRCQASFPYKGNLASHKTVHGEKPYKCNICGAQNPANLKTHT 593
 DB 317 D-SLVPGEDEKPYKCOLCRSSFRYKGNLASHKTVHGEKPYKCNICGAQNPANLKTHT 375
 QY 594 RIHSGEKPYKCEFCGAFVQVAVLRAVLIHTEKPYPCICGTRPRHLQTLKSHLRIHT 653
 DB 376 RIHSGEKPYKCEFCGAFVQVAVLRAVLIHTEKPYPCICGTRPRHLQTLKSHLRIHT 435
 QY 654 GEKPYHCEKCNLHFRHKSQRLHLRQKGAITTKYQYRV 693
 DB 436 GEKPYHCDPCGLHFRHKSQRLHLRQKGAITTKYQYRV 475
 RESULT 14
 ID AB064323 standard; protein; 479 AA.
 XX
 AC AB064323;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE AAC2-2 protein.
 XX
 KM Angiogenesis; cancer; AAC2-1; AAC2-2; tumour antigen; expression vector;
 KM cytostatic; gene therapy.
 OS Unidentified.
 XX
 PN WO2003080800-A2.
 PN 02-OCT-2003.
 PD 20-MAR-2003; 2003WO-US008536.
 PF 20-MAR-2002; 2002US-0365982P.
 PR (AVET) AVENTIS PASTEUR INC.
 PA
 PI Berinestein N, Lovitt C, Parrington M, Pedyczak A, Radvanyi L;
 PI Singh-Sandhu D;
 XX
 DR WPI: 2003-779251/73.
 DR N-PSDB; AAL56278.
 XX
 PT New expression vector for preventing or treating an angiogenesis-

PT dependent disease (e.g. breast cancer) comprises a nucleic acid sequence
 PT that encodes the angiogenesis-associated antigen AAC2-1 or AAC2-2.

XX Claim 50, Page 57, 57pp; English.

XX The present invention relates to an expression vector for inducing an
 CC anti-tumour response in a patient. Also provided is a method of
 CC using a vector to treat angiogenesis-dependent diseases. The
 CC composition and methods are useful in diagnosing, preventing, prognosing
 CC or treating an angiogenesis-dependent disease, preferably a breast
 CC cancer. The DNA molecule and protein may also be used in drug screening
 CC assays. The present invention is an AAC2 protein sequence shown in the
 CC exemplification of the invention

XX Sequence 479 AA:

Query Match 30.5%; Score 1155; DB 7; Length 479;
 Best Local Similarity 38.3%; Pred. No. 2,9e-80;
 Matches 268; Conservative 58; Mismatches 142; Indels 232; Gaps 15;

QY 1 MASP--DSCI---QFTRASDVLTNLRSDLTITVTVVYSRQFAHKTVMACS 54
 DB 1 MGPAPREGALGYRRETRHSSDVLGNLRLGLITVTVLVGGQPLRAHRAVLIAOS 60
 QY 55 GLPYSIFTDQKCNLAVINDPEINPEFCITLDFMYTSRLNREGNIMAVATAMYLQM 114
 DB 61 GFPTYSIFRGRAGGVVLSLPGPEARGFAPLIDFMYTSRLNREGNIMAVATAMYLQM 120
 QY 115 EHVVDTCRKFIRKASEAMVSAIKRPREEFNLNMLPDIIMAYRGREVENNLPLRSAPG 174
 DB 121 EHVVAQCHRFQAS----- 134
 QY 175 CERRAPAPSLVSLSTPPASYSMYSHLPVSSILFSEBEFRDVMFANPPEKRALPCDS 234
 DB 135 -----YEPRLGIS----- 141
 QY 235 ARPVEYSRPTLEVPVCHSNISPKETIPREASDMHVSVAELKPAAPGARAPAYF 294
 DB 142 -----LRLP----- 145
 QY 295 PCDKASKEERPSSEDEIALHFPNPAPLNRKGLVSPSPQSKDCQPNSPTEACSKMAC 354
 DB 146 -----EAPPT-----PPTAP-----PPGSPRRSEGHDPPTESRS----- 176
 QY 355 ILQASGSPPAKSPTPDPKACWKYKFTYVNSLQNAKPGPEADLGRISPRAYTPAPAC 414
 DB 177 ---CSGQPPSPAPDPDPKACWKYKFTYVNSLQNAKPGPEADLGRISPRAYTPAPAC 223
 QY 415 QPMEPENDLQSPPTKLSASGEDSTIP-QASRLNINIVNSMTGSPSSSESHSPLYMHP 473
 DB 224 QALPBGDEASSSSSSSSSESGPIPGPSRL-----SPTAATVQF----- 265
 QY 474 KCTSCGSPQAHMCLHTAGPTFAEMGTSYSDSCENGAFPCNECDKPSSEASL 533
 DB 266 ---KCG--APASTPYLLTSQ---AQTSGSPSERAPLPGSEFSCQNCCEAAGCSSGL 316
 QY 534 KRRTLTQHSKPKYKCDRCQASFRYKGNLSHKTVTHGKRYRNCNIGAOVRNPAKTKTH 593
 DB 317 D-SLVGDEDEKPYKCOLCRSSFRYKGNLSHKTVTHGKRYRNCNIGAOVRNPAKTKTH 375
 QY 594 RHSGEKPYKCTCGARFVVAHRAVHLHTGKPYKCEICGTRFRHLQTLKSHRIHT 653
 DB 376 RHSGEKPYKCTCGARFVVAHRAVHLHTGKPYKCEICGTRFRHLQTLKSHRIHT 435
 QY 654 GEXPHYCEKCNLHFRHNSQLRLHLRQGAITNTKYQVRY 693
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RESULT 15
 ADN38698
 ID ADN38698 standard; protein; 479 AA.
 XX

AC ADN38698;
 XX 17-JUN-2004 (first entry)

XX Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:16.

XX Human; differential expression; cancer; angiogenic disorder;
 KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
 KW inflammatory disease; autoimmune disease;
 KW retinal neovascularisation syndrome; scarring; uterine fibroid;
 KW detection; diagnosis; prognosis; drug screening; drug targeting;
 KW wound healing; contraception; cytostatic; cardiac; immunomodulatory;
 KW vulnereary; gene therapy; vaccine.

XX Homo sapiens.

XX WO2003042661-A2.

XX 22-MAY-2003.

XX 13-NOV-2002; 2002MO-US036810.

XX 13-NOV-2001; 2001US-0350666P.

XX 21-NOV-2001; 2001US-0332464P.

XX 29-NOV-2001; 2001US-0334393P.

XX 03-DEC-2001; 2001US-0335394P.

XX 14-DEC-2001; 2001US-0340376P.

XX 08-JAN-2002; 2002US-0347211P.

XX 10-JAN-2002; 2002US-0347349P.

XX 08-FEB-2002; 2002US-0356714P.

XX 13-FEB-2002; 2002US-0359077P.

XX 20-FEB-2002; 2002US-0368099P.

XX 29-MAR-2002; 2002US-0370110P.

XX 04-APR-2002; 2002US-0372246P.

XX 12-APR-2002; 2002US-0386614P.

XX 05-JUN-2002; 2002US-0396839P.

XX 16-JUL-2002; 2002US-0397775P.

XX 22-JUL-2002; 2002US-0397845P.

XX 09-SEP-2002; 2002US-0409450P.

XX (EOSB-) EOS BIOTECHNOLOGY INC.

XX Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevez PA;

XX Mack DH, Murray R, Watson SR, Wilson KE, Zlotnick A;

XX WPI; 2003-468649/44.

XX N-PSDB; ADN38697.

XX Determining the presence or absence of a pathological cell in a patient,

XX useful for diagnosing, prognosing or treating cancer, comprises detecting

XX a nucleic acid in a biological sample.

XX Claim 12; SEQ ID NO 16; 1385pp; English.

The invention relates to nucleic acids and proteins (ADN38698-ADN40064)
 CC whose expression is upregulated or downregulated in specific cancers or
 CC other diseases such as angiogenic or fibrotic disorders, and to methods
 CC of determining the presence or absence of a pathological cell in a
 CC patient by detecting a nucleic acid at least 80% identical to those of
 CC the invention or by detecting a polypeptide of the invention. The
 CC invention also relates to expression vectors and host cells comprising a
 CC nucleic acid of the invention; antibodies which specifically bind a
 CC polypeptide of the invention; use of such antibodies for drug targeting;
 CC and methods of screening for modulators of activity or expression of the
 CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
 CC antibodies and methods are useful for diagnosing, prognosing and treating
 CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
 CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
 CC neovascularisation syndromes, scarring and uterine fibroids. They may
 CC also be useful in wound healing and in contraception. The present
 CC sequence represents a polypeptide of the invention.

SQ Sequence 479 AA:

Query Match 30.5%; Score 1155; DB 7; Length 479;
 Best Local Similarity 38.3%; Pred. No. 2.9e-80;
 Matches 268; Conservative 58; Mismatches 142; Indels 232; Gaps 15;

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DB	61	GFTYSTIRGAGVGVVLSLPGCEHARGFAPLIDFMTSRNLSPATAPAVLAATLQM	120
QY	115	EHVYDTCRKFIKASEAMVSAIKPREEFLNSRMLMPQDIMAYRGREVENNLELRSAFG	174
DB	121	EHVYQACHRFIQAS-----	134
QY	175	CEBRAPAPSLYSGISTPPASYSMYSHLPVSSLPSDEFPRDVMVPANPPKERALPCDS	234
DB	135	-----YEPGIS-----	141
QY	235	ARPVGEYSRPTLEVSINVCNSIYSPKETIPPEARSDMYSAEGLKPAAPARNAPYF	294
DB	142	-----LRPL-----	145
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QY	355	ILQASGSPPAKSPTPDPAACWKKYKTYVLNSLNONAKPGCEQNELGRLSPRAYTAPAC	414
DB	177	---CSQGPSPSPAPDPACWKKYKTYVLNS-----QASQAGSLVGERSSGQPCP	223
QY	415	QPMPEPNTLQSPTKLSAGEDSTIP-QASRLNNIVNRSMWGSPPRSSSESHSPLYMHP	473
DB	224	QARLPSSDEASSSSSSSSSEBGPPIPGOSRL-----SPTATVQF-----	265
QY	474	KCTSCGSQSPQHAEMCLHTAGPTFAEMGETOSEYSDSSCENGAFPCNECDCRFSEASL	533
DB	266	---KCG--APASTPYLLTSQ---AODTSGSPSERARPLPGEFFSCQNGCEAVAGSSGL	316
QY	534	KRHTLQTHSDKPYKCDRCQASFRYKGNLASHKTYVHTGKPYKCNICGAQFNRPANLKTHT	593
DB	317	D-SLVPGDEDKPYKQCLCRSSFRYKGNLASHRTVHTGKPYKCSICGARFNRPANLKTHTS	375
QY	594	RIHSGEKPYKCTCGAPVVOVAHLRAVHLHTGKPYKCEICGTRFRHLQTLKSHLRHT	653
DB	376	RIHSGEKPYKCTCGSRFVOVAHLRAVHLHTGKPYKPCPTGTRFRHLQTLKSHVRHT	435
QY	654	GEKPYHCEKNLAFPHKSQLRLHLROKGAITNTKVOYRV	693
DB	436	GEKPYHCDPCGLMFRHKSQRLHLRQKGAATNTKVVHVI	475

Search completed: March 2, 2006, 03:49:45
 Job time : 192 secs

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GenCore version 5.1.7
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OM protein - nucleic search **using frame plus p2n model**

Run on: March 2, 2006, 00:18:39 ; Search time 9653 Seconds

(without alignments)
4157.410 Million cell updates/sec

Title: US-10-755-889-18

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Scoring table: BLOSUM62

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Ygapop 10.0	Ygapext 0.5
Fgapop 6.0	Fgapext 7.0
Delop 6.0	Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/abs/asstsrp.spool/us10755889/runat_01032006_143941_11251/app_query.fasta_1
-DB=GenEmbl -QWt=faetap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=bloum62 -TRANS=human40.cdi -LIST=45
-LOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abse07
-USER=us10755889 @CGN 1.1 4939 @runat 01032006 143941 11251 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THRAD=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database:

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2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
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7: gb_ph:*
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9: gb_ro:*
10: gb_ats:*
11: gb_sy:*
12: gb_un:*
13: gb_vt:*
14: gb_ncg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3793	100.0	3536	6	AR117606 Sequence
2	3793	100.0	3536	6	CS035889 Sequence
3	3793	100.0	3536	6	CS044841 Sequence

4	3793	100.0	3536	6	AR559323
5	3793	100.0	3536	6	AX410625
6	3793	100.0	3536	8	U00115
7	3777	99.6	2499	8	HSZNFNRA
8	3777	99.6	3630	6	CS031305
9	3777	99.6	3630	6	CS040257
10	3763	99.2	3720	6	AR142448
11	3763	99.2	3720	6	I49950
12	3763	99.2	3720	6	AR577709
13	3750	98.9	2600	6	S67779
14	3619	95.4	2067	6	CQ715154
15	3617.5	95.4	4196	8	HSMB07105
16	3604.5	95.0	2210	9	MUSMB06
17	3604.5	95.0	3330	9	BC052315
18	3602.5	95.0	2373	6	AX306062
19	3602.5	95.0	2373	9	MM041465
20	3013	79.4	2634	5	AJ719545
21	2585.5	68.2	4536	5	BC084912
22	2566.5	67.4	4376	5	BC077915
23	2314	61.0	125395	8	AC072022
24	2192	57.8	2277	5	BC059515
25	2179	57.4	168505	14	AC080010
26	2151.5	56.7	196774	14	AC158397
27	2138.5	56.4	2112	5	AB197694
28	2107	55.5	183575	14	AC152786
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38	1155	30.5	3476	6	CQ989654
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41	1151.5	30.4	1932	8	AB076580
42	1151	30.3	3562	6	CQ989652
43	1122.5	29.6	1749	6	AX25044
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45	975.5	25.7	882	5	BX930024

ALIGNMENTS

RESULT 1
LOCUS AR117606 AR117606 3536 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 3 from patent US 6140125.
ACCESSION AR117606
VERSION AR117606.1 GI:14098512
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3536)
AUTHORS Taylor,J.K. and Cowser,L.M.
TITLE Antisense inhibition of bcl-6 expression
JOURNAL Patent: US 6140125-A 3 31-OCT-2000;
FEATURES
source 1..3536
Location/Qualifiers
1..3536 /organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 3.89e-135 Length: 3536
Score: 3793.00 Matches: 706
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0

AR559323 Sequence
AX410625 Sequence
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CS031305 Sequence
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AR142448 Sequence
I49950 Sequence 1
AR577709 Sequence
S67779 BCL5-CY82-H
CQ715154 Sequence
BX649185 Homo sapi
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AX306062 Sequence
U41465 Mus musculu
AJ719545 Gallus ga
BC084912 Xenopus 1
BC077915 Xenopus 1
AC072022 Homo sapi
BC059515 Dario rer
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AC158397 Mus muscu
AB197694 Takifugu
AC152786 Bos tauru
AC095940 Rattus no
CR847938 Zebrafish
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BX936445 Dario rer
BX005335 Zebrafish
AC034185 Homo sapi
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AK122893 Homo sapi
BC059404 Homo sapi
AB076580 Homo sapi
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BX930024 Gallus ga

US-10-755-889-18 (1-706) x AR117606 (1-3536)

QY 1 MetAlaSerProAlaIaSerCysIIeGlnPheThrAlaArgHisAlaSerAspValLeuLeu 20
DB 328 ATGGCTCGCGCGCTCAAGCTGTATCCAGTTCACCCGCGCATCCAGTATGTTCTTCTTC 387
QY 21 AsnLeuAsnArgLeuArgSerArgAspIleLeuThrAspValValIleValValSerArg 40
DB 388 AACCTTAATGCTCTCGAGTCAAGACATCTTAAGTGTATGTTGTCTTGTGTGACCGCT 447
QY 41 GluGlnPheArgAlaHisIleThrValLeuMetAlaCysSerGlyLeuPheTyrSerIle 60
DB 448 GAGCAGTTTGAAGCCCAATAAAGCTCTCATAGCTCGACAGTGGCTGTCTTATAGCATC 507
QY 61 PheThrAspGlnLeuIleCysAsnLeuSerValIleAsnLeuAspProGluIleAsnPro 80
DB 508 TTATACAGACCAAGTTTAATGCAACCTTAAGTATCATCTAGATCTCGATCAACCCCT 567
QY 81 GluGlyPheCysIleLeuLeuAspPheMetTyrThrSerArgLeuAsnLeuArgGluGly 100
DB 568 GAGGAGATTGCAATCTCTGAGCTTATGATACACATCTGAGCTCAATTGCGGAGAGGC 627
QY 101 AsnIleMetAlaValMetAlaThrAlaMetTyrLeuGlnMetGluHisValIleAspThr 120
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QY 121 CysArgIlePheIleIleValIleSerGluValGluMetValSerAlaIleIleYsProArg 140
DB 688 TGCCGGAAAGTTTATTAAGCCAGATGAAGACAGATGTTTCTGCCATCAAGCCCTCTCGT 747
QY 141 GluGlnPheLeuAsnSerArgMetLeuMetProGluAspIleMetAlaTyrArgGlyArg 160
DB 748 GAAAGATTCTTCAACACCGAGATGCTGATGCCCAACACATCATGCTTATCGGAGCTG 807
QY 161 GluValValGluAsnAsnLeuProLeuArgSerAlaProGlyCysGluSerArgAlaIle 180
DB 808 GAGGTGTGAGAAACAACCTGCCACTGAGAGAGCGCCCTGGTGTGAGACAGACCTTT 867
QY 181 AlaProSerLeuTyrSerGlyLeuSerThrProProAlaSerTyrSerMetTyrSerHis 200
DB 868 GCCCCAGCTGTATGAGTGGCTGTCCACACCGCCACCTCTTATTCATGTACAGCTCAC 927
QY 201 LeuProValSerSerLeuLeuPheSerAspGluGlnPheArgAspValAlaGlyMetProVal 220
DB 928 CTCCTGTGACAGCCCTCTCTCTCCGATGAGAGATTGCGAGATGTCGGAATGCCCTG 987
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QY 421 GluAsnLeuAspLeuGlnSerProThrIleYsLeuSerAlaSerGlyGluAspSerThrIle 440
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QY 581 AlaGlnPheAsnArgProAlaAsnLeuIleYsThrHisArgIleHisSerGlyGluIleYs 600
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QY 621 ValLeuIleHisThrGlyGlyIleYsProTyrProCysGluIleCysGlyThrArgPheArg 640
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QY 641 HisLeuGlnThrLeuIleYsSerHisLeuArgIleHisThrGlyGlyIleYsProTyrHisCys 660
DB 2248 CACCTTCAAGCTGTGAAGAGCCACTGCGAATTCACACAGAGAGAGAAACCTTACCAATTGT 2307
QY 661 GluIleCysAsnLeuHisPheArgHisIleYsSerGlnLeuArgLeuHisLeuArgGlnIleYs 680
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QY 681 HisGlyAlaIleThrAsnThrIleYsValGlnTyrArgValSerAlaThrAspLeuProPro 700
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QY 701 GluLeuProIleYsAlaCys 706
DB 2428 GAGCTCCCAAAAGCTGCTG 2445

RESULT 2
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LOCUS Sequence 5395 from Patent WO2005016962.
DEFINITION CS035889
ACCESSION CS035889
VERSION CS035889.1 GI:60733752
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Abbas, A., Clark, H., Ouyang, W., Williams, M. P., Wood, W. I. and Wu, T. D.
AUTHORS Compositions and methods for the treatment of immune related
TITLE diseases
JOURNAL Patent: WO 2005016962-A 5395 24-FEB-2005;
FEATURES
SOURCE location/Qualifiers
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/mol_type="unassigned DNA"
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Score: 3793.00 Matches: 706
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 6
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QY 361 SerProProAlaIleYserProThrAspProIleValAlaCysAsnTrpIleValTyrPhe 380
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Db	2008	CTCCCAAGCCACAGAAGCCGTCTATCCGGTGAGAAACCTATCGTTGGCAACATCTGAGG	2067
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Db	2068	GCCCAAGTTCACCGGACCGCACACCTGTAACCCACACTGAAATTCCTCTGGAGAGAG	2127
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Db	2128	CCCTACAAATCCGAACCTCGCGAGACCGAGATTGTACAGGTGGCCCACTCCGTCCTAT	2187
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Db	2188	GTGCTTATCCACACTGTGTGAGAACCCCTATCCCTGTGAATCTGTGGACCGTTTCGG	2247
Oy	641	HisIeuGlnThrLeuYserSerHisLeuArgLIleHisThrgLyGuLysProTyrlHisCyse	660
Db	2248	CACCTTCAGACTCGAAGAGCCACTCGGAATTCACACAGGAGAGAAACCTTACCATTTG	2307
Oy	661	GUlYsCYsaEntLeuHisrPheArgHisIlysSerGlnLeuArgLeuHisLeuArgGLNlys	680
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ACCESSION	CS044841		
VERSION	CS044841.1	GI:61851389	
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ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 Abbas,A., Clark,H., Ouyang,W., Williams,P.M., Wood,W.I. and Wu,T.D. Compositions and methods for the treatment of immune related diseases Patent: WO 2005019258-A 5395 03-MAR-2005; Genentech, Inc. (US) Location/Qualifiers 1..3536 /organism="Mus musculus" /mol_type="unassigned DNA" /db_xref="taxon:10090"		
JOURNAL			
FEATURES	source		
ORIGIN			
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Best Local Similarity:	100.0%	Mismatches:	0
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OY	101	AsnIleMetAlaValMetAlaThrAlaMetYrLeuGlnIleMetGluHisValValAspThr	120
Db	628	AACATCATGCTGTGATGATGCCAGCTATGTATCTGCAAGATGAGACATGTTGTGACACT	687
OY	121	CysArgIysPheIleIeIysAlaSerGluValGluMetValSerAlaIleIeYsProArg	140
Db	688	TGCGGAGATTATTAAGCGCCAGTGAACAGAGATGTTCTGACATCAAGCTCTCGT	747
OY	141	GluGluPheLeuAsnSerArgMetLeuMetProGlnAsp11leMetAlaTyrrArgIlyArg	160
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Db	988	GCAACCCCTTCCCAAGAGAGCGGCACTCCATGTGATGTGCGACAGCCACTCTGAT	104
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Db	1288	GCACCCCCTGAACCGGAGAGGCTGTGATTGTCCACAGAGCCCCCAGAAATCTGATCCACG	1344
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OY	361	SerProProAlaLysSerProThrAspProLysAlaCyAsnThrIlyIysTyIysPhe	380
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 Db 1588 GAGAACTTGACCTCCAGTCCCAACCAAGCTGAGTCCACGCGGAGGAGACTCCACCATC 1647
 Qy 441 ProGlnAlaSerAraGluAunAunIleValAsnArgSerMetThrGlySerProArgSer 460
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 Db 1948 CACAGTACAAACCTTACAGGTGACCGCTGACGAGGCTCTTCCGCTACAAAGGCAAC 2007
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 LOCUS AR559323
 DEFINITION Sequence 90 from patent US 6750015.
 ACCESSION AR559323
 VERSION AR559323.1 GI:53968739

KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE
 AUTHORS 1 (bases 1 to 3536)
 TITLE Horwitz, K.B. and Richter, J.
 JOURNAL Progestosterone receptor-regulated gene expression and methods related
 FEATURES
 source Patent: US 6750015-A 90 15-JUN-2004;
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 DEFINITION Sequence 3272 from Patent WO0229103.
 ACCESSION AX410625
 VERSION AX410625.1 GI:21443330
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 Homidae; Homo.
 REFERENCE
 1
 Alvarez, C., Horne, D., Perez-da-Silva, S. and Vockley, J. G.
 AUTHORS
 TITLE Gene expression profiles in liver cancer
 JOURNAL Patent: WO 0229103-A 3272 11-APR-2002;
 GENE LOCUS INC (US)
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 VERSION U00115.1 GI:392426
 KEYWORDS
 SOURCE
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 3536)
 Ye,B.H., Lister,F., Lo Coco,F., Knowles,D.M., Offit,K.,
 Chaganti,R.S. and Dalla-Favera,R.
 Alterations of a zinc finger-encoding gene, BCL-6, in diffuse
 large-cell lymphoma

JOURNAL Science 262 (5134), 747-750 (1993)
PUBMED 8235596
REFERENCE 2 (bases 1 to 3536)

AUTHORS Ye, B.H.
TITLE Direct Submision
JOURNAL Submitted (04-AUG-1993) Binhui Hilda Ye, Pathology, College of
Physicians & Surgeons of Columbia University, 630 W168th Street,
New York, NY 10032, USA

FEATURES Location/Qualifiers
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ORIGIN

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DB: 8 Gaps: 0

US-10-755-889-18 (1-706) x U00115 (1-3536)

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DEFINITION         H.sapiens mRNA for zinc finger protein.
ACCESSION          Z21943
VERSION            Z21943.1  GI:297025

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KEYWORDS LAZ-3 gene; zinc finger protein.

SOURCE Homo sapiens (human).

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 2499)

AUTHORS Kerckaert, J.P., Dewindt, C., Tilly, H., Quief, S., Lecocq, G. and Bagstad, C.

TITLE LAZ3, a novel zinc-finger encoding gene, is disrupted by recurring chromosome 3q27 translocations in human lymphomas

JOURNAL Nat. Genet. 5 (1), 66-70 (1993)

PubMed 8220427

REFERENCE 2 (bases 1 to 2499)

AUTHORS KERCKAERT, J.P.

TITLE Direct Submision

JOURNAL Submitted (02-MAR-1993) KERCKAERT J. P., INSERM U.124, Molecular Onco-Hematology, Place de Verdun, LILLE CEDEX, FRANCE, 59045

FEATURES

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ORIGIN

Alignment Scores:

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Query Match: 99.6% Indels: 0
DB: 8 Gaps: 0

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US-10-755-889-18 (1-706) x HSZNFNRPRA (1-2499)

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LOCUS CS031305 3630 bp DNA linear PAT 10-MAR-2005

DEFINITION Sequence 811 from Patent WO2005016962.
 ACCESSION CS031305
 VERSION CS031305.1 GI:60731413
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 AUTHORS Abbas, A.; Clark, H.; Ouyang, W.; Williams, M.P.; Wood, W.I. and Wu, T.D.
 TITLE Compositions and methods for the treatment of immune related diseases
 JOURNAL Patent: WO 2005016962-A 811 24-FEB-2005;
 Genentech, Inc. (US)

FEATURES
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 Location/Qualifiers
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Alignment Scores:
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Db	2221	CCCTACAAATCGAAACCTGGCGAGCCAGATTGTATACAGGTGGGCCACCTCCGTGCCAT	2280
Qy	621	ValIleuIleHisThrGlyGlyIysProTyrProCyseGluIleCyseGlyThrArgPheArg	640
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Qy	681	HisGlyAlaIleThrAsnThrIysValGlnIlyrArgValSerAlaThrAspLeuProPro	700
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DEFINITION	Sequence 811 from Patent WO2005019258.	linear	PAT 22-MAR-2005
ACCESSION	CS040257		
VERSION	CS040257.1	GI:61848078	
KEYWORDS			
SOURCE			
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	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
	Homnidae; Homo.		
REFERENCE	1		
AUTHORS	Abbas,A., Clark,H., Ouyang,W., Williams,P.M., Wood,W.I. and Wu,T.D.		
TITLE	Compositions and methods for the treatment of immune related diseases		
JOURNAL	Patent: WO 2005019258-A 811 03-MAR-2005;		
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Best Local Similarity:	99.6%	Mismatches:	2
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 ACCESSION ARI42448
 VERSION ARI42448.1 GI:15102747
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.

REFERENCE 1 (bases 1 to 3720)
 AUTHORS Chaganti, R.S.K. and Dalla-Favera, R.
 TITLE Cloning and uses of the genetic locus BCL-6
 JOURNAL Patent: US 6174997-A 1 16-JAN-2001;
 FEATURES location/Qualifiers
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 Db 508 TTTCACAGCAGGTTGAATCAACCTTAGTGTGATCATCTAGATCTGAGATCAACCT 567
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 Db 628 AACATCATGCTGTGATGCGCAGCGCTATGATCTGAGATGAGACATGTTGTGACACT 687
 Qy 121 CysArgIlePheIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 140
 Db 688 TGCCGAAAGTTTATTAAGCCAGTGAAGAGAGATGTTTCTGCCATCAAGCTCTCTCGT 747
 Qy 141 GlnGlnPheLeuAsnSerArgMetLeuMetProGlnAspIleMetAlaTyrArgGlyArg 160
 Db 748 GAAAGTTCCTCAACACCGGATGCTGATGCCCAAGACATCATGCGCTTATCGGAGTGT 807
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 Db 808 GAGGTGTGAGAAACAACCTGCCACTGAGAGAGCCCTTGGGTGTGAGAGAGAGCTTT 867
 Qy 181 AlaProSerLeuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 200
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Qy      301  LyGluGluGluGluArgProSerSerGluAspGluIleAlaLeuHisPheGluProProAn 320
Db      1228  AAGAGAGAGAGAGAGCCCTCTCCGAGATGATGATGATGATGATGATGATGATGATGATGAT 1287
Qy      321  AlaProLeuAsnArgLyGlyLeuValSerProGlnSerProGlnLySerAspCyGln 340
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Qy      461  SerSerGluSerHisSerProLeuTyMetHisProProLyCyGlyThrSerCyGlySer 480
Db      1708  AGCGCGAGAGCCACTACCACTCTACATGACCCCCCAAGGTGACAGTCTCTGGGCTCT 1767
Qy      481  GlnSerProGlnHisAlaGluMetCysLeuHisThrAlaGlyProThrPheAlaGlu 500
Db      1768  CAGTCCCAAGCAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1827
Qy      501  MetGlyLutThrGlnSerGluTyRSerAspSerSerCyGluAsnGlyAlaPhePheCys 520
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Qy      521  AsnGlyCyAspCyValArgPheSerGluGluAlaSerLeuLyAspGlyHisThrLeuGlnThr 540
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Qy      541  HisSerAspLySerProTyRlyAspAspArgCysGlnAlaSerPheArgTyRlyGlyAsn 560
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Qy      561  LeuAlaSerHisLySerThrValHisThrGlyLutLySerProTyRArgCysAsnIleCyGly 580
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Qy      661  GlyLyAspAsnLeuHisPheArgHisLySerSerGlnLeuArgLeuHisLeuArgGlyLys 680
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Qy      681  HisGlyAlaIleThrAsnThrLySerValGlnTyRArgValIleSerAlaThrAspLeuPro 700
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DEFINITION Sequence 1 from patent US 5641672.
ACCESSION 149950
VERSION    149950.1 GI:2472170
KEYWORDS   .
SOURCE      Unknown.
ORGANISM   Unknown.
REFERENCE   1 (bases 1 to 3720)
AUTHORS     Dalla-Favera, R. and Chaganti, R.S.K.
TITLE        Cloning and uses of the genetic locus bcl-6
JOURNAL      Patent: US 5641672-A 1 24-JUN-1997;
FEATURES     Location/Qualifiers
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DB:              Gaps:      0

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Qy      121  CysArgLyPheIleLyAlaSerGluAlaGluMetValSerAlaIleLySerProProArg 140

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 Db 1648 CCACAGGCGAGCGGCTCAATACATCGTTAACAGGTCACTACAGCGGCTCTCCCGGAGC 1707
 Qy 461 SerSerGlulSerHisSerProleuYrMetHisPProProlyCySThSerCysglYser 480
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RESULT 12
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 LOCUS AR577709 Sequence 1 from patent US 6783945.
 DEFINITION AR577709
 ACCESSION AR577709
 VERSION AR577709.1 GI:56580344
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 3720)
 AUTHORS Chaganti,R.S.K. and Dalla-Favera,R.
 TITLE Cloning and uses of the genetic locus bcl-6
 JOURNAL Patent: US 6783945-A 1 31-AUG-2004;
 The Trustees of Columbia University in the City of New York and
 Sloan-Kettering Institute for Cancer Research, New York, NY
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Query Match: 99.2% Indels: 0
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US-10-755-889-18 (1-706) x AR577709 (1-3720)

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RESULT 13

LOCUS 567779 2600 bp mRNA linear PRI 13-Apr-2001
DEFINITION BCL5=Cy2-His2 zinc-finger transcription factor [human, liver,
mRNA, 2600 nt].

ACCESSION 567779
VERSION 567779.1 GI:459372

KEYWORDS

SOURCE

ORGANISM Homo sapiens (human)

Homosapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE

1 (bases 1 to 2600)
Miki,T., Kawamata,N., Hirose,S. and Aoki,N.
Gene involved in the 3q27 translocation associated with B-cell
lymphoma, BCL5, encodes a Kruppel-like zinc-finger protein
Blood 83 (1), 26-32 (1994)

JOURNAL

PUBMED 8274740
GenBank staff at the National Library of Medicine created this
entry [NCBI gisbq 141975] from the original journal article.

REMARK

FEATURES

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/note="Cy2-His2 zinc-finger transcription factor;
sequence presented in paper contains a frameshift in the
coding region"

ORIGIN

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Score: 3750.00 Matches: 702
Percent Similarity: 99.6% Conservative: 1
Best Local Similarity: 99.4% Mismatches: 3
Query Match: 98.9% Indels: 1
DB: 8 Gaps: 0

US-10-755-889-18 (1-706) x 567779 (1-2600)

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QY 101 AsnIleMetAlaValMetAlaThrAlaMetTyrLeuGlnMetGlnHisValValAspThr 120
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QY 141 GlnGlnPheLeuAsnSerArgMetLeuMetProGlnAspIleMetAlaTyrArgGlyArg 160
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DB 1620 GGGCGCTTTCACAGAGCTTACAGGCCCCCACTGCTGCGCAGCAACCATGAGAGCT 1679
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DB 1680 GAGAACCTTGACCTCCAGTCCCAACCAAGGTGAGTCCAGGGGAGAGACTCCACATC 1739
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Qy 501 MetGlyGluThrGlnSerGluTyrSerAspSerSerCysGluGlnGlnValAlaPhePheCys 520
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Qy 621 ValLeuIleHisThrGlyGluLysProTyrProCysGluIleCysGlyThrArgPheArg 640
Db 2280 GTGCTTATCCACACTGCTGAGAGAGCCCTATCCCTGTAATCTGTGGCACCCCTTCCGG 2339
Qy 641 HisLeuGlnThrLeuLysSerHisLysArgTyrLeuThrGlyGluLysProTyrHisCys 660
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CQ715154
DEFINITION Sequence 1088 from Patent WO02068579.
ACCESSION CQ715154
VERSION CQ715154.1 GI:42276011
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, B.W.
TITLE Kites, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 1088 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES
SOURCE location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.: 8,47e-129 Length: 2067
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US-10-755-889-18 (1-706) x CQ715154 (1-2067)

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 Homnidae; Homo.
 1 (bases 1 to 4196)
 Lauber, J., Bahr, A., Mewes, H.W., Weil, B., Aml, C., Oeanger, A.,
 Fobo, G., Han, M. and Wiemann, S.
 The German Human cDNA Consortium
 Direct Submission
 Submitted (26-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764
 Neuherberg, GERMANY
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
 sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
 consortium of the German Genome Project.
 This clone (DKFZp686M22130) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcententrum, Heubnerweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
 information about the clone and the sequencing project is available
 at <http://mips.gsf.de/proj/cDNA/>.
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US-10-755-889-18 (1-706) x HSM807105 (1-4196)

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QY 580 IYAlaGlnPheAsnArgProAlaAsnLeuIleThrHisThrArgIleHisSerGlyGluL 600
Db 2726 GGGCCAGTTCAACCGGCAAGCCCACTGAACCAACCACTGAAATTCATCTGAGAGAA 2785
QY 600 YProTyrrIleCysGlyThrProCysGlyAlaIleArgPheValIleHisIleuArgAlaH 620
Db 2786 AGCCCTTCAAAATGCGAAACCTGGAGGCGCAAGTTGTACAGGTTGGCCACCTTCGTGCC 2845
QY 620 IeValIleuIleHisThrGlyGluIleYProTyrrProCysGlyIleCysGlyTyrrArgPhea 640
Db 2846 ATGTGCTTATTCACATGCTGTGAGAACCTTATCCCTGTGAATCTGTGCAACCCGTTTCC 2905
QY 640 rGHisIleuGlnThrIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 660
Db 2906 GGCACCTTCAAGCTGAGAGAGCCACTGCAATCCACACAGAGAGAAACCTTACCATT 2965
QY 660 YGlyIleCysCysAsnLeuHisPheAsnGlnHisIleuSerGlnIleuArgLeuHisIleuArgGluL 680
Db 2966 GTGAGAGAGTGAACCTGCAATTCCTGCAAAAGAGGCTGCACTTCCGCGCAGAA 3025
QY 680 YHisIleGlyAlaIleThrAsnTrpIleValIleGlnTyrrArgValSerAlaThrAspLeuProP 700
Db 3026 AGCATGGCCCATCAACCAACCAAGTGCATACCGCGTGTACAGCACTGACCTCCTC 3085
QY 700 rGluIleuProIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 720
Db 3086 CGAGCTCCCAAAAGCTCTG 3105

Search completed: March 2, 2006, 03:08:00
Job time : 9697 secs

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PF 15-OCT-1999; 99US-00418640.
XX B-cell CLL/lymphoma 6, zinc finger protein 51 and IAZ3) is a sequence-
PR 15-OCT-1999; 99US-00418640.
XX (ISIS-) ISIS PHARM INC.
PA Taylor JK, Cowseart LM,
PI WPI, 2001-048959/06.
XX P-PSDB; AAB29640.
DR
XX
PT Antisense compounds which specifically hybridize with and inhibit human
PT bcl-6 expression, useful for treating bcl-6 related disorders, and
PT preventing or delaying inflammation or tumor formation.
PS
XX
XX Claim 1; Col 45-52; 42pp; English.
XX This sequence represents cDNA encoding human bcl-6. Bcl-6 (also known as
CC B-cell CLL/lymphoma 6, zinc finger protein 51 and IAZ3) is a sequence-
CC specific DNA-binding transcriptional repressor. The bcl-6 gene is
CC expressed in germinal centre B- and T- cells and is required for germinal
CC centre formation and Th-2 mediated antibody affinity maturation. Bcl-6
CC may also play a role in the regulation of apoptosis. The bcl-6 gene is
CC located on chromosome 3q27, a region which undergoes a high frequency of
CC translocation events. Such chromosomal translocations can result in
CC aberrant forms of bcl-6, which are strongly implicated in the
CC pathogenesis of several types of lymphoma, and have also been reported in
CC acute lymphoblastic leukaemia and post-transplant lymphoproliferative
CC disorders. The invention relates to antisense oligonucleotides targeted
CC to the human bcl-6 gene, which inhibit its expression. A series of
CC oligonucleotides (AAC8144-C81223) were designed to target different
CC regions of the human bcl-6 mRNA, and were analysed for their effect on
CC bcl-6 mRNA levels by quantitative real-time PCR. The oligonucleotides of
CC the invention are useful for diagnosis, prevention and treatment of
CC conditions associated with aberrant forms of bcl-6, such as lymphomas,
CC acute lymphoblastic leukaemia and post-transplant lymphoproliferative
CC disorders
XX
SQ Sequence 3536 BP; 936 A; 943 C; 835 G; 822 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1,4e-192 Length: 3536
Score: 3793.00 Matches: 706
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0

US-10-755-889-18 (1-706) x AAC81137 (1-3536)
QY 1 MetAlaSerProAlaAaPseCySlleGlnPheThrArgHisAlaSerAapValIleuLeu 20
DB 328 ATGCCCTCCGCGGCTGACAGCTGTATCCAGTTCACCCGCATGCACTGATGTTCTTCTC 387
QY 21 AsnIeuAanArgIeuAaGSeSerArgAaPslIleuThrAapValIleValIleValIle 40
DB 388 AACCTTAATGCTCTCCGAGTCCAGACATCTTAAGTATGTTGATTTGATGGACCT 447
QY 41 GluInIleuAaArgAlaHisAluYsThrValIleuMeAlaCySeSerGlyIeuPheTySerIle 60
DB 448 GAGCAGTTTGAAGCCCAATAAAGGTCCTCATGCGCTGACGTGCGCTGTTCTATAGCATC 507
QY 61 PheThrAaPslIleuLeuYsCyAaenIeuSerValIleAaenIeuAaPProGluIleAaenPro 80
DB 508 TTTACACACACAGTTGAATGCAACCTTAAGTGTATCATCTAGATCCTGAGATCAACCT 567
QY 81 GluInIleuAaArgAlaHisAluYsThrValIleuMeAlaCySeSerGlyIeuPheTySerIle 100
DB 568 GAGGAGTTCGACATCCCTCGACTTCATGACATCTCGGCTCAATTGCGGAGGAGG 627
QY 101 AsnIleuMeAlaValIleMeAlaThrAlaMeTyIleuGlnIleuGlnIleValIleAaPThr 120
DB 628 AACATCATGCTGTGATGGCCACCGCTATGTAAGTCTGACGATGAGCATGTTGTGGAAC 687

QY 121 CysArgIysPheIleAlaSerGluAlaGluMetValSerAlaIleuYsProProArg 140
DB 688 TCCCGAAGTTTATTAAGGCCAGTGAAGCAGAGATGTTTCTGCCATCAAGGCTCTCGT 747
QY 141 GluInIleuAaSerArgIeuMetIeuMetProGlnAaPslIleuThrArgGlyArg 160
DB 748 GAAAGATTCCTCAACAGCCGAGTGTGATGCCCAAGCATCATGAGCTATGCGGAGTCT 807
QY 161 GluValIleAlaAaenIleuProIeuAaGSeSerAlaAProGlyCyGlnSerArgAlaPhe 180
DB 808 GAGGTGGTGAAGAAACCTGCACTGAGAGACGCTCGGAGTGTGAGAGCAGACCTT 867
QY 181 AlaProSerIeuTySerGlyIeuSerThrProProAlaSerTySerMetTySerHis 200
DB 868 GCCCCAGCTTACATGAGTGGCTGTCCACACGCCAGGCTTATTCATGACAGCCAC 927
QY 201 IeuProValIleSerIleuIeuPheSerAaPslGluInIleuAaArgAaPValArgMetProVal 220
DB 928 CTCCTGTGACAGACTCTCTTCTCCGATGAGAGTTTCGGAGATGTCGGAGTGCCTGTG 987
QY 221 AlaAaenProPheProGlyGluArgAlaIleuProCyAaPseSerAlaArgProValProGly 240
DB 988 GCCAACCTTTCGCCAAGAGGCGGCACTCCATGTGATGATGCCAGGCAAGTCTGCT 1047
QY 241 GluTySerArgProThrIleuGluValSerProAaenValCyHisSerAaenIleTySer 260
DB 1048 GAGTACAGCCGCGCCACATTTGAGAGTGTCCCAATGTGTGCAACAGAAATCTATTTCA 1107
QY 261 ProGlyGluThrIleProGluGluAlaArgSerAaPheHisTySerValAlaGluGly 280
DB 1108 CCCAAGAAACATCCAGAAAGAGCAGCAAGATGATGACATTAAGTGTGCTAGAGGCT 1167
QY 281 IeuYsProAlaAlaProSerAlaArgAaenAlaProTyIlePheProCyAaPslYsAlaSer 300
DB 1168 CTCAAACCTGCTGCCCTTCAAGCCGAAATGCCCCCTATCTTCCTGTGACAAAGCCAC 1227
QY 301 IysGluGluGluArgProSerSerGluAaPslIleAlaIleuHisPheGluProProAaen 320
DB 1228 AAGAGAAAGAGAGACCTCTCTCGAAGATGAGATTCCTGCTGATTCAGGCCCCCAAT 1287
QY 321 AlaProIeuAaAaArgIysGlyIeuValSerProGlnSerProGlnIleYsSerAaPcyGln 340
DB 1288 GCAACCTGTAACCGGAAGGCTGTGTTAGTCCACAGAGCCCCAGAAATCTGACTGCGAG 1347
QY 341 ProAaenSerProThrGluAlaCySeSerIysAaenAlaCyHisIleuGlnIleSerGly 360
DB 1348 CCCAACTCCGCCACAGAGGCTGACAGCAGTAAGATGCTGCATCTCCAGGCTCTTGCC 1407
QY 361 SerProProAlaIleYsSerProThrAaPProGlyAlaCyAaenTrpYsIleYsPhe 380
DB 1408 TCCCTCTCAGCCAAAGAGCCCACTAGACCCCAAGCTGCACTGAAAGAAATACAAATTC 1467
QY 381 IleValIleuAaSerIeuAaGlnAaenAlaIleYsProGlyIleProGluGlnAlaGluLeu 400
DB 1468 ATGTGCTCAACAGCTTCAACAGATGCCAAACAGGAGGAGCTGAGAGGCTGAGCTG 1527
QY 401 GlyArgIeuSerProArgAlaIleTyThrAlaProProAlaCyGlnIleProPheMetGluPro 420
DB 1528 GGCCTGCTTTCGCCAAGACCTTACAGGCCCCACCTGCTGCAGACCCATGAGAGCT 1587
QY 421 GluAaenIleuAaPslIleuIleSerProThrIleYsSerAlaSerGlyIleAaPseThrIle 440
DB 1588 GAGAACCTTGACCTCCAGATCCCAACCAAGCTGAGTGCAGCGGAGAGACTCCACATC 1647
QY 441 ProGlnAlaSerArgIeuAaAaenIleValAaAaSerMetThrGlySerProArgSer 460
DB 1648 CCAACAGCCAGCGGCTCATATAACATGTTTACAGGTCCATGACGAGCTCTCCCGCAGC 1707
QY 461 SerSerGluSerHisSerProIeuTyIleMetHisProProGlyCyHisTySerGlyYsSer 480
DB 1708 AGCAGGAGAGCAGCACTACACATCTACATGACCCCCCGAAGTGCAGTCTCGGAGCT 1767

[illegible]

XX	PF	03-OCT-2001; 2001MO-US030821.
XX	PR	03-OCT-2000; 2000US-0237199P.
XX	PA	(GENE-) GENE LOGIC INC.
XX	PI	Beazer-Barclay Y., Weisman SM, Yamaga S, Vockley J;
XX	DR	WPI, 2002-435528/46.
XX	PT	Detecting granulocyte activation by detecting differential expression of
XX	PR	genes associated with granulocyte activation, which serves as diagnostic
XX	PT	markers that is useful for monitoring disease states and drug toxicity.
PS	XX	Claim 1; SEQ ID NO 745; 114bp; English.
CC	XX	The invention relates to detecting (M1) granulocyte (GC) activation
CC	XX	(GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC	XX	DNA chip analysis as given in the specification, and comparing the
CC	XX	expression level to an expression level in an unactivated GC, where
CC	XX	differential expression of Gs is indicative of GCA. Also included are
CC	XX	modulating (M2) GA by contacting GC with an agent that alters the
CC	XX	expression of at least one gene in Gs; (2) screening (M3) for an agent
CC	XX	capable of modulating GCA or an inflammation (especially chronic) in a
CC	XX	tissue, an allergic response in a subject, exposure of a subject to a
CC	XX	pathogen or sterile inflammatory disease using the gene expression
CC	XX	profile; (3) detecting (M4) an inflammation (especially chronic) in a
CC	XX	tissue, an allergic response in a subject, exposure of a subject to a
CC	XX	pathogen or sterile inflammatory disease, by detecting the level of
CC	XX	expression in a sample of the tissue of gene(s) from Gs, where the level
CC	XX	of expression of the gene is indicative of inflammation; (4) treating
CC	XX	(M5) an inflammation (especially chronic) or in a tissue, an allergic
CC	XX	response in a subject, exposure of a subject to a pathogen or sterile
CC	XX	inflammatory disease, by contacting a tissue having inflammation with an
CC	XX	agent that modulates the expression of gene(s) from Gs in the tissue. M1
CC	XX	is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful
CC	XX	for screening an agent capable of modulating GCA preferably in an
CC	XX	inflammation in a tissue; M4 is useful for detecting an inflammation
CC	XX	(especially chronic) in a tissue, an allergic response in a subject,
CC	XX	exposure of a subject to a pathogen or sterile inflammatory disease (e.g
CC	XX	psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis,
CC	XX	cardiac reperfusion injury, renal reperfusion injury, ARDS, adult
CC	XX	respiratory distress syndrome, inflammatory bowel disease, Crohn's
CC	XX	disease, ulcerative colitis, periodontal disease; also bacterial
CC	XX	infection, viral infection, parasitic infection, protozoal infection,
CC	XX	fungal infection and M5 is useful for treating one of the above
CC	XX	conditions. The present sequence represents a gene differentially
CC	XX	expressed in granulocytes. Note: The sequence data for this patent did
CC	XX	not form part of the printed specification, but was obtained in
CC	XX	electronic format directly from WIPO at
CC	XX	ftp.wipo.int/pub/published_pct_sequences
SQ	XX	Sequence 3536 BP; 936 A; 943 C; 835 G; 822 T; 0 U; 0 Other;
Alignment Scores:		
Pred. No. :	1,4e-192	Length: 3536
Score:	3793.00	Matches: 706
Percent Similarity:	100.0%	Conservative: 0
Best Local Similarity:	100.0%	Mismatches: 0
Query Match:	100.0%	Indels: 0
DB:	6	Gaps: 0
US-10-755-889-18 (1-706) x ABR84174 (1-3536)		
QY	1	MetAlaSerProAlaAspSerCysIleGlnPheThrArgHisAlaSerAspValLeuLeu 20
Db	328	ATGGCGTTCGCCGCTACAGCTGTATTCAGATTACCCGCGCATCGCAGTAGTTCTTCTC 38
QY	21	AenLeuAsnArgLeuArgSerArgAspLlleuThrAspValValIleValValSerArg 40
Db	388	AACTTAATTCGTCCTCCGAGTCAGACATCTTGACTGATGTTTGTCATTTGTGAGCGGT 44
QY	41	GIUGInPheArgAlaHisIlyStrHrVallLeuMeAlaCysSerGlyLeuPheTySerIle 60

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Db 448 GAGCATTAGAGCCATAAAGCTCTCATGCGCTGAGGTGCTGTTCTATAGACATC 507
Qy 61 PheThrAspGlnLeuLysCysAsnLeuSerValIleAsnLeuAspProGluIleAsnPro 80
Db 508 TTATACAGACCAAGTTGAAATGCAACTTAGTGATCAATCTAGATCCTAGATCAACCTCT 567
Qy 81 GluGlyPheCysIleLeuLeuAspPheMetTyrThrSerArgLeuAsnLeuArgGlnGly 100
Db 568 GAGGAGTTCTGACATCTCTGAGCTTCAATGATACATCTCGCTCAATTTGGCGGAGGGC 627
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Db 628 AACATATGCTGTGATGCGCAAGGCTATGATCTGCAATGAGATGAGCATGTTGGACACT 687
Qy 121 CysArgLysPheIleLysValAspGlnValGlnMetValSerAlaIleLysProArg 140
Db 688 TGCAGAAAGTTTATTAAGGCAAGTGAAGCAGAGATGGTTCTGCCATCAAGCCTCTCGT 747
Qy 141 GluGluPheLeuAsnSerArgMetLeuMetProGlnAspIleMetAlaTyrArgGlyArg 160
Db 748 GAAAGATTCTTCAACAGCCGAGATGCTGATGCCCAAGACATCAATGGCTATCGGGATCGT 807
Qy 161 GluValValGluAsnAsnLeuProLeuArgSerAlaProGlyCysGlnSerArgAlaPhe 180
Db 808 GAGTGGTGAACAACACTGCCACTGAGAGAGCGCCCTGGGTGTGAGCAGAGCCTT 867
Qy 181 AlaProSerLeuTyrSerGlyLeuSerThrProProAlaSerTyrSerMetTyrSerHis 200
Db 868 GCCCCGAGCTGTACAGTGGCTGTCCACACCGCCAGCCTTATTTCCAGTACACCCAC 927
Qy 201 LeuProValSerSerLeuLeuPheSerArgGlnGluPheArgAspValArgMetProVal 220
Db 928 CTCCCTGTACAGACCTCTCTCTCTCCGATGAGAGATTTGGAGATGCCGATGCCGTG 987
Qy 221 AlaAsnProPheProLysGlnArgAlaLeuProCysAspSerAlaArgProValProGly 240
Db 988 GCCAACCCCTTCCCAAGAGAGCGGAGCCTCCCAATGTGATGTGCGAGCGACGCTCGGT 1047
Qy 241 GluTyrSerArgProThrLeuGlnValSerProAsnValCysHisSerAsnIleTyrSer 260
Db 1048 GAGTACAGCCGCGCGCATTTGAGGTGTCCCCCAATGTGCGACAGCAATATCTATTTCA 1107
Qy 261 ProLysGlnThrIleProGlnGlnAlaArgSerAspMetHisTyrSerValAlaGlnGly 280
Db 1108 CCAAGGAACAAATCCCAAGAGAGCGACAGATGATATGCACTACATGTGGCTGAGGAGC 1167
Qy 281 LeuLysProAlaAlaProSerAlaArgAsnAlaProTyrPheProCysAspLysAlaSer 300
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Qy 301 LysGlnGlnGlnArgProSerSerGlnAspGlnIleAlaLeuHisAspGlnProProAsn 320
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Qy 321 AlaProLeuAsnArgLysGlyLeuValSerProGlnSerProGlnLysSerAspCysGln 340
Db 1288 GCAACCCCTGAACCGAAAGGCTGTGTTATGTCACAGAGCCCCCAAGATCTGATGCGAG 1347
Qy 341 ProAsnSerProThrGlnAlaCysSerSerLysAsnAlaCysIleLeuGlnAlaSerGly 360
Db 1348 CCAAACTCGCCCAAGAGGCTGAGACATGAAATCTCTGACCTCCAGGCTTCCGCGC 1407
Qy 361 SerProProAlaLysSerProThrAspProLysAlaCysAsnTrpLysTyrLysPhe 380
Db 1408 TCCCTCTCAGCAAGAGACCCCACTGACCCCAAGCCTGCAACTGGAAGAATATCAAGTTC 1467
Qy 381 IleValLeuAsnSerLysLeuAsnGlnAsnAlaLysProGlyGlyProGlnGlnAlaGlnLeu 400
Db 1468 ATCGTGTCAACAGCCTCAACAGAAATGCCAAACAGAGGGGCTGTGAGAGGCTGAGACTG 1527
Qy 401 GlyArgLeuSerProArgAlaTyrThrAlaProProAlaCysGlnProMetGlnPro 420

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Db 1528 GGCCTGCTTCCCAAGAGCCTTACAGCGGCCCACTGCTGCGACCACTCATGAGCCT 1587
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Qy 441 ProGlnAlaSerArgLeuAsnAsnIleValAsnArgSerMetThrGlySerProArgSer 460
Db 1648 CCACAAGCCAGCGGCTCAATACATCGTTAACAGGTCCATGACAGGCGGCTCTCCGCGAGC 1707
Qy 461 SerSerGlnSerHisSerProLeuTyrMetHisProProLysCysThrSerCysGlySer 480
Db 1708 ACCAGCGAGGCACTCAACCACTTACATGACACCCCGAAATGACAGCTCTGCGGCTCT 1767
Qy 481 GlnSerProGlnHisAlaGlnMetCysLeuHisThrAlaGlyProThrPheAlaGlnGlu 500
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Qy 501 MetGlyGlnThrGlnSerGlyLysSerAspSerCysGlnAsnGlyAlaPhePheCys 520
Db 1828 ATGGGAGAGACCAAGCTGAGTACTCAATCTTACCTGTGAGAGACGGGCTTCTTCTGCG 1887
Qy 521 AsnGluCysAspCysArgPheSerGlyGlnAlaSerLysLeuValArgHisThrLeuGlnThr 540
Db 1888 AATGAGTGTGACTGCGCTTCTCTGAGAGGCTCTCATCMAAGGACACGCTGACAGACC 1947
Qy 541 HisSerAspLysProTyrLysCysAspArgCysGlnAlaSerPheArgTyrLysGlyAsn 560
Db 1948 CACAGTGAACAAACCTTACAGATGTGACCGCTCCAGGCTCTTCCGCTACAAAGGGCAAC 2007
Qy 561 LeuAlaSerHisLysThrValHisThrGlyGlnLysProTyrArgCysAsnIleCysGly 580
Db 2008 CTGCGACGACCAAGACCGTTCATACCGGTGAGAAACCTATCGTTGCAACATCTGTGGG 2067
Qy 581 AlaGlnPheAsnArgProAlaAsnLeuLysThrHisThrArgIleHisSerGlyLysLys 600
Db 2068 GCCCAGTTCAACCGGCACAGCACTGAAACCCACACTCGAATTCACTTGAGAGAGAG 2127
Qy 601 ProTyrLysCysGlnThrCysGlyAlaArgPheValGlnValAlaHisLeuArgAlaHis 620
Db 2128 CCTACAAATGGAAACCTGCGAGGCAAGATTTGTACAGTGGCCACCTCGTGCCAT 2187
Qy 621 ValLeuIleHisThrGlyLysLysProTyrProCysGlnIleCysGlyThrArgPheArg 640
Db 2188 GTGCTTATCAACATGTGTGAAGAGCCCTATCCCTGTGAATCTGTGGCACCGTTCGCG 2247
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Qy 681 HisGlyAlaIleThrAsnThrLysValGlnTyrArgValSerAlaThrAspLeuProPro 700
Db 2368 CATGGCGCATCACCAACACCAAGTGAATACCGGTGTGAGCCACTGACCTGCTCGG 2427
Qy 701 GluLeuProLysAlaCys 706
Db 2428 GAGCTCCCAAGCCTGC 2445

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RESULT 3
 ABN96774 standard; DNA; 3536 BP.
 ID ABN96774
 XX
 AC ABN96774;
 XX
 DT 13-AUG-2002 (first entry)
 XX
 DE Gene #3272 used to diagnose liver cancer.
 XX
 KM Gene; liver cancer; de; hepatocellular carcinoma; hepatotropic;

KW metastatic liver tumour; cytostatic; expression profile; disease state;
KW disease progression; drug toxicity; drug efficacy; drug metabolism.
OS Homo sapiens.
PN M0200229103-A2.
XX
XX 11-APR-2002.
XX PD 02-OCT-2001; 2001WO-US030589.
XX PF 02-OCT-2000; 2000US-0237054P.
XX PR (GENE-) GENE LOGIC INC.
XX PA Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;
XX PI WPI; 2002-426119/45.
XX DR
XX PT Diagnosing and detecting the progression of liver cancer, hepatocellular
XX PT carcinoma or metastatic liver tumor in a patient, involves detecting the
XX PT level of expression of two or more genes in a liver tissue sample.
PS Claim 1; SEQ ID NO 3272; 298bp; English.
XX
XX The invention relates to a novel method for diagnosing and detecting the
XX CC progression of liver cancer, hepatocellular carcinoma or metastatic liver
XX CC tumour in a patient, and differentiating metastatic liver cancer from
XX CC hepatocellular carcinoma in a patient, involving detecting the level of
XX CC expression of two or more genes represented in ABN93503-ABN97455 in a
XX CC tissue sample. The method of the invention has hepatocytic, and
XX CC cytosolic activity. The method is useful for diagnosing and detecting
XX CC the progression of liver cancer, hepatocellular carcinoma and metastatic
XX CC liver carcinoma in a patient. The method is useful for identifying
XX CC expression profiles which serve as useful diagnostic markers as well as
XX CC markers that can be used to monitor disease states, disease progression,
XX CC drug toxicity, drug efficacy and drug metabolism. Note: The sequence data
XX CC for this patent did not form part of the printed specification, but was
XX CC obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 3536 BP; 936 A; 943 C; 835 G; 822 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1,4e-192 Length: 3536
Score: 3793.00 Matches: 706
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0
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QY 1 MetAlaSerProAlaIlePheSerCysIleGlnPheThrArgHISAlaSerAspValIleuLeu 20
DB 328 ATGAGCTTCGCGGCTGACAGCTGATCCAGTTCACCCGCCAATGCGAGATGTTCTTCTC 387
QY 21 AsnIleuAsnArgIleuArgSerArgAspIleuThrAspValIleValIleValSerArg 40
DB 388 AACCTTAATCGTCTCCGAGTGCAGACATCTTGACTGATGTTGTCATTGTTGTGAGCCGT 447
QY 41 GluGlnPheArgAlaIleValThrValIleuMetAlaCysSerGlyIleuPheTyrSerIle 60
DB 448 GAGCAGCTTAAAGCCCAATAAACGCTCTCAATGGCTCCAGTGGCTTTCTAATGACATC 507
QY 61 PheThrAspGlnIleuLeuPheCysAsnIleuSerValIleAsnIleuAspProGlnIleAsnPro 80
DB 508 TTACAGACACAGTGAATAATGCAACTTATGATGATCAATCAATCCAGAGATCAACCT 567
QY 81 GluGlyPheCysIleIleuLeuAspPheMetTyrThrSerArgIleuAsnIleuArgGlyIle 100
DB 568 GAGGATTTCTGCATCTCTCGAGCTTCAATGATACATCTCGGCTCAATTTGCGGAGGAGC 627

QY 101 AsnIleMetAlaValMetAlaThrIleMetTyrLeuGlnMetGlnIleValIleAspThr 120
DB 628 AACATCATGGCTTGTATGATGCGACAGCTATATCTTCAATGAGATGATGTGGACACT 687
QY 121 CysArgIlePheIleValIleAsnArgIleuValIleuMetValSerAlaIleIlePheProArg 140
DB 688 TGCCGAGAGTTTATTAAGCCAGATGAAAGAGATGATGTTCTGCTCAATCAAGCTCTCCGT 747
QY 141 GluGlnPheLeuAsnSerArgPheMetLeuMetProGlnIleMetAlaTyrArgGlyArg 160
DB 748 GAAGAGTTCCTCAACAGCCGAGATGTGATGCCCAAGACATCAATGAGCTTATCGGAGCT 807
QY 161 GluValIleGluAsnIleuPheLeuArgSerAlaProGlyCysGluSerArgAlaPhe 180
DB 808 GAGTGTGTGAAGAACACTGCTGACAGAGAGGCCCCCTGGGTGTGAGACAGACCTT 867
QY 181 AlaProSerLeuTyrSerGlyIleuSerThrProProAlaSerTyrSerMetTyrSerHis 200
DB 868 GCCCCAGCCTGTACAGTGGCTGTCCACACCCGACCTCTTATTCATGACAGCCAC 927
QY 201 LeuProValSerSerIleuLeuPheSerArgPheGluGlnPheArgAspValArgMetProVal 220
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DB 1048 GAGTACAGCCGCGCGACTTGTGAGGTGTCCCAATGTGTGCCACAGCAATATCTAATCA 1107
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DB 1108 CCNAGGAACATATCCAGAAAGAGCGACGAAGATGTGATCACTACGTGTGCTGACAGGCG 1167
QY 281 LeuIleProAlaIleProSerAlaArgAsnAlaProTyrPheProCysAspIleValSer 300
DB 1168 CTCAACCTCTGCTCCCTTCAAGCCGAAAGCCCCCTACTTCCCTTGTGACAGGCGAGC 1227
QY 301 LysGluGlnIleuArgProSerSerGluAspGlnIleAlaIleuHisPheGluProProAsn 320
DB 1228 AAGAGAAAGAGAGACCTCTCTCGAAGATGAGATGCTCCGTGATTTGAGGCCCCCAAT 1287
QY 321 AlaProIleuAsnArgIleuValIleSerProGlnSerProGlnIleuSerAspCysGln 340
DB 1288 GCACCCCTGAAACGGAGAGGCTGTGTTAGTCCACAGAGCCGCCAGAAATCTGACTGCGAG 1347
QY 341 ProAsnSerProThrGlnIleuValCysSerSerIleAsnAlaCysIleIleuGlnIleSerGly 360
DB 1348 CCCAACTCGCCCAACAGAGGCTGTGACAGATGATGCTGCACTTCAGGCTTGTGC 1407
QY 361 SerProProAlaIleuSerProThrAspProIleuValIleCysAsnIleuTyrIlePhe 380
DB 1408 TCCCTCTCAAGCCAGAGCCCACTGACCCCAAGCCCTGCACTGAGAAATCAAGATTC 1467
QY 381 IleValIleuAsnSerIleuAsnIleuAsnAlaIlePheProGlnIleuValIleGlnIleu 400
DB 1468 ATGCTGTCAACAGCTCAACAGATGCCAAACCAAGGAGGCGCTGAGAGGCTGAGAGCTG 1527
QY 401 GlyArgIleuSerProAlaGlnIleTyrThrAlaProProAlaCysGlnProPheMetGluPro 420
DB 1528 GCGCGCTTTCCTCCACAGAGCTTCAACGCGCCCACTGCTGCGCAGCCACCATGAGACCT 1587
QY 421 GluAsnIleuAspIleuGlnSerProThrIleuLeuSerAlaSerGlyIleuAspSerThrIle 440
DB 1588 GAGAACCTTGAACCTTCACTGCCCAACCAAGCTGATGTCAGCGGAGAGATCAACATC 1647
QY 441 ProGlnIleSerArgIleuAsnAsnIleValIleAsnArgSerMetThrGlySerProArgSer 460
DB 1648 CCAACAGCCAGCGGCTCAATTAACATGTTAAACAGTCCATGACGAGGCTCTCCCGGACGC 1707
QY 461 SerSerIleuSerHisSerProIleuTyrMetHisProProIleuSerCysThrSerCysGlySer 480

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Db      1708 AGCAGGAGAGGACCACTACCACTCTACATGCAACCCCGAAGGACAGCTCTCGGCTCT 1767
Qy      481 GInserProGlnHISalagUwecYgLeuHISThAlagIyProThrPhealagIuGlu 500
Db      1768 CAGTCCCAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1827
Qy      501 MetGlgIuThrcInserGluYrserAapserSerCygluAnslgIuAlaPhePheCys 520
Db      1828 ATGGAGAGAGCCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1887
Qy      521 AasnGluCyAspCyAspArgPheSerGluGluAlaSerLeuYsArgHISThrLeuGlnTrir 540
Db      1888 AATGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1947
Qy      541 HISerAapIyPProTyrIyCyAspArgCygluAlaSerPheArgTyrIygluAan 560
Db      1948 CACAGTGAACAAACCTTACAAAGTGAACCGCTGACAGGCTCTTCCGCTACAAAGGCAAC 2007
Qy      561 LeuAlaSerHISerHISerThValHISerHISerHISerHISerHISerHISerHISerHISer 580
Db      2008 CTGCGACGACCAAGACCGCTGATACCGGTGAAGAAACCTTATGCTGCAATCTGAGAGAG 2067
Qy      581 AlAGInPheAsnArgProAlaAsnLeuYsThrHISerHISerHISerHISerHISerHISerHISer 600
Db      2068 GCCAAGTTCACCGGCGACGACCACTGAAACCAACCACTGAAATTCATCTGAGAGAGAG 2127
Qy      601 ProTyrIyCygluThrcYgIyAlaArgPheValGlnValAlaHISerHISerHISerHISer 620
Db      2128 CCTTCAAAATGCGAAACCTGCGAGCGAATTTGTACAGTGGCCCACTCTGCGCCAT 2187
Qy      621 ValLeuHISerHISerHISerHISerHISerHISerHISerHISerHISerHISerHISerHISer 640
Db      2188 GTGCTTATCCACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2247
Qy      641 HISerHISerHISerHISerHISerHISerHISerHISerHISerHISerHISerHISerHISer 660
Db      2248 CACCTTCAAGCTGGAAGACCACTGCGATCAACAGAGAGAAACCTTACATTTG 2307
Qy      661 GluIyCyAsnLeuHISerHISerHISerHISerHISerHISerHISerHISerHISerHISer 680
Db      2308 GAGAGAGTGAACCTGATTCCTGCAAAAGCCAGCTGCGATTCATTCCTGCGCCCAAGAG 2367
Qy      681 HISGlyAlaIleThrPheThrIyValGlnTyrArgAlaSerAlaThrAapLeuProPro 700
Db      2368 CATGGCCGATCAACCAACAGGTGATACCGGTGACGACTGACCTGCTCG 2427
Qy      701 GluIyProIyAlaCys 706
Db      2428 GAGCTCCCAAGCTGCTC 2445

RESULT 4
ID ADR14016 standard; DNA; 3536 BP.
XX
AC ADR14016;
XX
DT 21-OCT-2004 (first entry)
XX
DB Human NF-kappaB pathway-associated gene Segid17.
XX
XX NF-kappaB pathway; antiinflammatory; cytosolic; hepatotropic; virocidic;
XX antiarthritic; antirheumatic; gastrointestinal-gen; antiaslomatic;
XX antiatherosclerotic; immunomodulator; cerebroprotective; vasotrophic;
XX immunosuppressive; vulnery; gene therapy; immune disorder;
XX inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;
XX hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;
XX hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;
XX X-linked anhidrotic ectodermal dysplasia; immunodeficiency;
XX viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;
XX rheumatoid arthritis; host cell survival; evasion of immune response;
XX atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;

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KM autoimmune disorder; hyper immune activity;
KM aberrant acute phase response; hypercongenital condition; birth defect;
KM necrotic lesion; wound; organ transplant rejection;
KM aberrant signal transduction; proliferating disorder; cancer;
KM HIV propagation; gene; ds; human.
OS Homo sapiens.
PN MO2004065577-A2.
PD 05-AUG-2004.
PF 13-JAN-2004; 2004WO-US000739.
PR 14-JAN-2003; 2003US-044068P.
PR 12-MAY-2003; 2003US-0469757P.
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
PI Nadler SG, Neubauer MG, Feder JN, Carman J;
DR WPI, 2004-562168/54.
DR P-PSDB; ADR14017.
XX New isolated polynucleotides and polypeptides associated with NF-kappaB
XX pathway, useful for diagnosing, treating, or preventing disorders or
XX diseases associated with NF-kappaB pathway.
XX Claim 1, SEQ ID NO 17, 237pp; English.
XX
XX This invention relates to the novel association of protein sequences (and
XX the genes which encode them) to the NF-kappaB pathway. The invention may
XX be useful for the production of compounds with an antiinflammatory,
XX cytosolic, hepatotropic, virocidic, antiarthritic, antirheumatic,
XX gastroenteric, immunomodulator, cerebroprotective, vasotropic, immunosuppressive or
XX immunomodulator, cancer, aberrant apoptosis,
XX related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,
XX hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM
XX syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic
XX ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,
XX hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell
XX survival, evasion of immune responses, rheumatoid arthritis, inflammatory
XX bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick
XX syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper
XX immune activity, disorders related to aberrant acute phase response,
XX hypercongenital conditions, birth defects, necrotic lesions, wounds,
XX organ transplant rejection, conditions related to organ transplant
XX rejection, disorders related to aberrant signal transduction,
XX proliferating disorders, cancers and HIV propagation in cells infected
XX with other viruses. The present sequence is that of a human gene which is
XX CC subject to the novel association with the NF-kappaB pathway of the
XX CC invention. Note: This sequence does not appear in the specification but
XX was obtained by the indexer from Genbank.
XX
XX SO Sequence 3536 BP; 936 A; 943 C; 835 G; 822 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1,4e-192 Length: 3536
Score: 3793.00 Matches: 706
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0

US-10-755-889-18 (1-706) x ADR14016 (1-3536)
Qy 1 MetAlaSerProAlaAspSerCygluGlnPheThrArgHISAlaSerAapValLeuLeu 20
Db 328 ATGAGCTCCGCGGCTGACAGCTGATCCAGTTCACCCGCGACGATGATGATTTCTTCTC 387

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QY	21	AsnLeuAsnArgLeuArgSerArgAspIleLeuThrAspValValIleValSerArg	40
Db	388	AACTTATATGTCCTCCGGAGTCCAGACATCTTGACGTATGTTGCATGTTGTGAGCGCT	447
QY	41	GlulInpHeuArgAlaHisIlyeThrValLeuMetAlaCysSerGlyLeuPheTyrSerIle	60
Db	448	GAGCAGTTTGAAGCCCATTAACCGATCTCATAGGCCGACAGTGCCCTGTTCTATAGCATC	507
QY	61	PheThrAspGlnLeuLysCysAsnLeuSerValIleAsnLeuAspProGlnIleAsnPro	80
Db	508	TTTACACACCAAGTTGAATGCACACTTAAGTGTATCATGTAGTCTGTGATCAACCTT	567
QY	81	GlulGlyPheCysIleLeuLeuAspPheMetTyrThrSerArgLeuAsnLeuArgGluGly	100
Db	568	GAGGAGATTCTGCATCTCTCTGACTCATATGTACATCTGGCTCATTTGGCGGAGGCG	627
QY	101	AsnIleMetAlaValMetAlaThrIleMetTyrLeuGlnMetGlnHisValIleAspThr	120
Db	628	AACTATATGGCTGTGATGGCCACGGCTATGTACTGCAGATGAGAGCATGTTGTGACACT	687
QY	121	CysArgIlyPheIleIlyeValSerGlnAlaGlnMetValSerAlaIleIlyeProProArg	140
Db	688	TGCGGAAAGTTATTAAAGGCCAGAGAGACAGAGATGTTTCTGCCATCAAGCCCTCCGCT	747
QY	141	GlulInpHeuLeuAsnSerArgMetLeuMetProGlnAspIleMetAlaTyrArgGlyArg	160
Db	748	GAAGAGTTCTCCACACGCGGATCTGATGCCCCAAGACATCAAGGCTTATCGGGAGCT	807
QY	161	GluValValGluAsnAsnLeuProLeuArgSerAlaProGlyCysGlnSerArgAlaPhe	180
Db	808	GAGGTGTGGAGAACACACTGCCACTGAGAGGCCCTGGGTGTGAGAGAGAGCTTT	867
QY	181	AlaProSerLeuTyrSerGlyLeuSerThrProProAlaSerTyrSerMetTyrSerHis	200
Db	868	GCCCCAGCCTGTACAGTGAGGCTGTCCACACGACCTCTTATTCACATGACAGCAC	927
QY	201	LeuProValSerSerLeuLeuPheSerAspGlnIlePheArgAspValArgMetProVal	220
Db	928	CTCCCTGTACACAGCTCTCTCTCTCCCATAGAGATTCGGAGATGCCGATGCTCGTG	987
QY	221	AlaAsnProPheProLysGluArgAlaLeuProCysAspSerAlaArgProValProGly	240
Db	988	GCCACACCCCTTCCCGAGAGAGCGGACATCCCAATGTATGTGCCAGGCCAGTCCCTGCT	1047
QY	241	GluTyrSerArgProThrLeuGlnValSerProAsnValCysHisSerAsnIleTyrSer	260
Db	1048	GAGTACAGCCGCGCCACTTTGAGAGTGTCCCAATGTGTGCCACAGAAATATCATTTCA	1107
QY	261	ProLysGlnThrIleProGlnGlnAlaArgSerAspMetHisTyrSerValIleGluGly	280
Db	1108	CCCAAGGAACATCTCCAGAGAGGCAAGAGTATATGCACTACATGATGTGGCTGAGAGGC	1167
QY	281	LeuLysProAlaAlaProSerAlaArgAsnAlaProTyrPheProCysAspLysAlaSer	300
Db	1168	CTCAAACTGTGTGCCCTCCCTCAGCCCGGAATCCCTCTTCCCTGTGACAAAGCCAGC	1227
QY	301	LysGlnGlnIleArgProSerSerGlnAspGlnIleAlaLeuHisPheGlnProProAsn	320
Db	1228	AAAGGAAGAGAGAGCCCTCTCTCCGAATATGATGTGCTCTGCAATTTGCAGCCCCCAAT	1287
QY	321	AlaProLeuAsnArgLysGlyLeuValSerProGlnSerProGlnLysSerAspCysGln	340
Db	1288	GCACCCCTGAACCGGAAGGATGTGTATGTCCACAGAGCCCCCAGAAATCTGATGCGCAG	1347
QY	341	ProAsnSerProThrGlnAlaCysSerSerLysAsnAlaCysIleLeuGlnAlaSerGly	360
Db	1348	CCCAACTGCCCCACAGAGCCCTGCAGCAGATAGATGTCTGTATCTCCAGGCTTCTGGC	1407
QY	361	SerProProAlaLysSerProThrAspProLysAlaCysAsnTyrLysTyrLysPhe	380
Db	1408	TCCCTTCAGCCAGAGGCCCACTAATCCCAAGCCTGCACTGAGAAATACAAATTC	1467

OY	381	ILleValIleuMseRleuAangIlnaRnAlaIySProGlyGlyProGluGlnAlaGluLeu	400
Db	1468	ATCTGTCTCAACAGCCTTCAACCGAATGCGCAACCGAGGGGCGCTTAGCAGCGCTGAGCTG	1527
OY	401	GlyArgLeuSerProATGAlaTATYThrAlaProProAlaCysGlnProPromeGluPro	420
Db	1528	GGCGGCGCTTTCACGAGCGCTTACGCGGCCCACTGTCGTCGACGCAACCATGAGCCT	1587
OY	421	GluAsnLeuApleuGlnSerProThrLYLeuSerAlaSerGlyGluApsSerThrIle	440
Db	1588	GAGAACCTTGAACCTCCAGTCCCGCCCAACCAAGCTGATGTCGACGCGGGAGGACTCCACATC	1647
OY	441	ProGlnAlaSerAArgLeuAaMaRnIleValAsnArgSerMetThrGlySerProArgSer	460
Db	1648	CCACAGCGCAGCGCGGCTCAATTAACATGCTTAAACAGGTCAAGAGGAGCTCTCCCGCAGC	1707
OY	461	SerSerGlnSerHisSerProLeuTYMetHisProProLYScyThrSerCysGlySer	480
Db	1708	AGCAGCGAGAGCCACTACCACTTACATGACACCCCGCGAAGTSCAGTCTCGGGCTCT	1767
OY	481	GlnSerProGlnHisAlaGluMetCysLeuHisIsthAlaGlyProThrPheAlaGluGlu	500
Db	1768	CAGTCCCGCAGCATGACAGAGATGTCCTCCACACCGCTGGCCCGCAGTTCGCTGAGAG	1827
OY	501	MetGlyGluThrGlnSerGluTYSerApsSerSerCysGluAangIyAlaPhePheCys	520
Db	1828	ATGGGAGAGACCCAGCTGAGTACTCATGATTTCTAAGCTGTGAACCGGAGCGCTTCTTGC	1887
OY	521	AangIuCYAaAPCyAATpPheSeGlyGlnAlaSerLeuIyAArgHisIsthLeuGlnThr	540
Db	1888	AATGAGTGTGATCGCGCTTCTCTGAGAGGCGCTCATCAAGAGGACACAGCTGCAACC	1947
OY	541	HisSerAapLYProTYLYScyAaAPArgCysGlnAlaSerPheArgTYLYGlyAsn	560
Db	1948	CACAGTGCACAAACCTTCAAGTGTGACGCTGCAGGCGCTCTCCGCTCAAGAGGCAAC	2007
OY	561	LeuAlaSerHisLYIsthValHisIsthGlyGluLYProTYArgCYAaenIleCYGly	580
Db	2008	CTCGCGACCGCCACAGACCGTCCATACCGGTGAGAAACCTTATCGTTGCACATCTGAGG	2067
OY	581	AlaGlnPheAaArgProAlaAsnLeuLYIsthHisIsthArgGlieHisSerGlyGlyLYs	600
Db	2068	GCCCGAGTTCACCGGCGCAGCACTGTAAACCCACACTGAAATTCATCTCGAGAGAG	2127
OY	601	ProTYLYScyGluThrCYGlyAlaArgPheValGlnValAlaHisLYLeuArgAlaHis	620
Db	2128	CCCTTCAAAATCGAAACCTGCGAGGACGAGATTTGTACAGGTGGCCACCTCGAGCCAT	2187
OY	621	ValLeuIleHisIsthGlyGluLYProTYProCYSeGlyIleCYGlyThrArgPheArg	640
Db	2188	GGGCTTATTCACACTGTGTGAGAAACCCCTATCCCTGTGAATCTGTGGACCCGTTCCGG	2247
OY	641	HisLeuGlnIsthLeuLYSerHisLYLeuArgGlieHisIsthGlyGluLYProTYHisCYs	660
Db	2248	CACCTTCAGACTGTGAAGGCACTGTGAATTCACACAGGAGAGAAACCTTACATTGT	2307
OY	661	GluLYScyAaenLeuHisPheArgHisLYSerGlnLeuArgLeuHisLYLeuArgGlyLYs	680
Db	2308	GAGAAAGTAACTGATTTCTCGTACAAAAGCCAGCGTGGCATTCCTTGGCGCAGAG	2367
OY	681	HisGlyAlaIleIsthAsnThrLYValGlnTYArgValSerAlaIsthAapLeuProPro	700
Db	2368	CATGGCGCCATCACAACCAAGGTGAATACCGCGTGCAGGCACATGACTGCTGCTCG	2427
OY	701	GluLeuProLYValaCYs 706	
Db	2428	GAGCTCCCGCAAGCCTGC 2445	

XX 21-OCT-2004 (first entry)
XX
XX Human NF-kappaB pathway-associated gene SeqID65.
XX
XX NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;
XX antituberc; antirheumatic; gastrointestinal-Gen; antiaesthetic;
XX antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;
XX immunosuppressive; vulnery; gene therapy; immune disorder;
XX inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;
XX hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;
XX hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;
XX X-linked andidrotic ectodermal dysplasia; immunodeficiency;
XX viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;
XX viral replication; host cell survival; evasion of immune response;
XX rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;
XX atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;
XX autoimmune disorder; hyper immune activity;
XX aberrant acute phase response; hypercongenital condition; birth defect;
XX necrotic lesion; wound; organ transplant rejection;
XX aberrant signal transduction; proliferating disorder; cancer;
XX HIV propagation; gene; de; human.
XX
XX Homo sapiens.
XX
XX MO2004065577-A2.
XX
XX 05-AUG-2004.
XX
XX 13-JAN-2004; 2004MO-US000798.
XX
XX 14-JAN-2003; 2003JUS-0440068P.
XX 12-MAY-2003; 2003JUS-0469757P.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
XX Nadler SG, Neubauer MG, Feder JN, Carman J;
XX WPI, 2004-562168/54.
XX P-PSDB; ADRI4065.
XX
XX New isolated polynucleotides and polypeptides associated with NF-kappaB
XX pathway, useful for diagnosing, treating, or preventing disorders or
XX diseases associated with NF-kappaB pathway.
XX
XX Claim 1, SEQ ID NO 65; 237bp; English.
XX
XX This invention relates to the novel association of protein sequences (and
XX the genes which encode them) to the NF-kappaB pathway. The invention may
XX be useful for the production of compounds with an antiinflammatory,
XX cyostatic, hepatotropic, virucide, antituberc, antiaesthetic,
XX gastrointestinal-Gen, antiaesthetic, antiarteriosclerotic,
XX immunomodulator, cerebroprotective, vasotropic, immunosuppressive or
XX immunoregulatory activity or for gene therapy. The proteins and nucleotides are
XX useful for diagnosing, preventing, treating, or ameliorating conditions
XX or diseases associated with the NF-kappaB pathway. The condition is an
XX immune disorder, an inflammatory disorder, an inflammatory disorder
XX related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,
XX hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM
XX syndromes, hypohidrotic ectodermal dysplasia, X-linked andidrotic
XX ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,
XX hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell
XX survival, evasion of immune responses, rheumatoid arthritis, inflammatory
XX bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick
XX syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper
XX immune activity, disorders related to aberrant acute phase responses,
XX hypercongenital conditions, birth defects, necrotic lesions, wounds,
XX organ transplant rejection, conditions related to organ transplant
XX rejection, disorders related to aberrant signal transduction,
XX proliferating disorders, cancers and HIV propagation in cells infected
XX with other viruses. The present sequence is that of a human gene which is
XX subject to the novel association with the NF-kappaB pathway of the
XX invention. Note: This sequence does not appear in the specification but

CC was obtained by the indexer from Genbank.
XX
XX Sequence 3536 BP; 936 A; 943 C; 835 G; 822 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 1,4e-192 Length: 3536
Score: 3793.00 Matches: 706
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 13 Gaps: 0
US-10-755-889-18 (1-706) x ADRI4064 (1-3536)
QY 1 MetAlaSerProAlaAspSerCysIleGlnPheThrArgHisAlaSerAspValIleuLeu 20
DB 328 ATGGCTCCCGCGGACGCTGATCCAGTTCCAGTCCCGCATGCGATGATTTCTTCTC 387
QY 21 AenLeuAsnArgLeuArgSerArgAspIleLeuThrAspValIleValIserArg 40
DB 388 AACCTTAATCGTCTCGGAGTGAAGACATCTTGACTGATGTTGATTTGTGAGCGGT 447
QY 41 GluGlnPheArgAlaHisIleThrValIleuMetAlaCysSerGlyLeuPheTyrSerIle 60
DB 448 GAGCAGTTTAGAGCCCATTAACGGTCCCTCATGGCTGAGGCTGAGGCTGTTCTATGACATC 507
QY 61 PheThrAspGlnIleuLeuPheAsnIleuSerValIleAenLeuAspProGluIleAsnPro 80
DB 508 TTACAGACCACTGATGAATGCAACCTTAGTGATCATCTGATCTGATGATCAACCTT 567
QY 81 GluGlyPheCysIleLeuLeuAspPheMetTyrThrSerArgLeuAsnLeuArgGluGly 100
DB 568 GAGGATTCGTGATCTCTCTGACATTCATGACATCTCGGCTCAATTTGCGGAGGCG 627
QY 101 AenIleMetAlaValIleMetAlaThrAlaMetCylTyrLeuGlnMetGluHisValIleAspThr 120
DB 628 AACATCATGGCTGTGATGAGCCAGGCTATGATCTGACATGAGACATGTTGTGACACT 687
QY 121 CysArgGlyPheIleIleValIleSerGluIleGluMetValIleValIleAspProArg 140
DB 688 TGCCGGAAGTTATTAAGGCGCATGAGAGAGATGTTTCTGCCATCAAGCTCTCTGCT 747
QY 141 GluGluPheLeuAsnSerArgMetLeuMetProGlnAspIleMetAlaTyrArgGlyArg 160
DB 748 GAAAGATTCCTCAACAGCCGATGCTGATGCCCAAGACATCATGCGGATCGCT 807
QY 161 GluValIleValIleAsnAsnLeuProIleuArgSerAlaProGlyCysGluSerArgAlaPhe 180
DB 808 GAGGTGTGAGAACCACTGCGACCTGAGAGACGCGCTTGGTGTGAGAGAGAGCTTT 867
QY 181 AlaProSerLeuTyrSerGlyIleuSerThrProProAlaSerTyrSerMetTyrSerHis 200
DB 868 GCCCCAGGCTGTACAGTGGCCCTGTCCACAGCGGCGCTCTTATTCATGTAAGCCAC 927
QY 201 LeuProValSerSerLeuLeuPheSerAspGluGluPheArgAspValIleArgMetProVal 220
DB 928 CTCCTCTGACAGAGCTCTCTCTTCTCCGATGAGAGTTCCGGAGTCCGGATGCTGTG 987
QY 221 AlaAsnProPheProIleGluArgAlaIleuProCysAspSerAlaArgProValProGly 240
DB 988 GCCAACCCCTTCCCAAGAGAGCGGACATCCCATGTGATGCGGCGGACAGTCCCTGT 1047
QY 241 GluTyrSerArgProThrIleuGluValIleSerProAsnValCysHisSerAsnIleTyrSer 260
DB 1048 GAGTACAGCGGCGGACCTTTGAGGTGTCCCAAGTGTGTCCACAGCAATATCTATTCA 1107
QY 261 ProIleGluThrIleProGluGluAlaArgSerAspMetHisTyrSerValAlaGluGly 280
DB 1108 CCCAAGAAACATCCCAAGAGAGCAAGAGATGATGACATCACTGATGCTGAGGCG 1167
QY 281 LeuLeuProAlaIleProSerAlaArgAsnAlaProTyrPheProCysAspIleValIleSer 300
DB 1168 CTAAACCTGTGCGCCCTCAGCGGAAATGCGCCCTTACTTCCCTGTGACAAAGCGCAGC 1227

QY	301	LYSGIUGIUGIUGRGP	PROSE	SESGIUA	ASGIULI	ELIALEUHI	ISPHEGIUGI	PRO	CAEN	330
Db	1228	AAAGAGAGAGAGAG	ACCTCTCT	CGAAGATG	AGATTGCC	TGATTTCC	AGACCC	CCCAAT	1287	
QY	321	AlaProLeu	AsnArgLysGlyLeu	ValSerPro	GlnSerPro	GlnLysSer	AspCys	Gln	340	
Db	1288	GCAACCTCGAAC	CGGAGGGCTGGT	TAGTCCAC	AGACCCCA	GAATCTGACT	CGCAG	1347		
QY	341	Pro	AsnSerPro	ThrGlnVal	CysSerSer	LysAsnAla	CysAlileu	GlnAla	350	
Db	1348	CCCAACTCGCCCA	AGAGGCGCTG	AGCAATG	ATCCCTG	CACTCCAG	GCTTCTTG	GC	1407	
QY	361	Se	ProProAla	LysSerPro	ThrAspPro	LysAlaCys	AsnTrpLys	TrpLysPhe	380	
Db	1408	TCCCTTCAG	CGAAGAGCCCA	CTGACCCCA	AGCCTG	CAACTG	AGAATAC	CAAGTTTC	1467	
QY	381	Ile	ValLeu	AsnSerLys	Leu	AsnAlaLys	AspGlyPro	GlnGlnAla	400	
Db	1468	ATCTGTCTCA	ACACCTTCA	CCAGAAAGCC	AAACAG	GGGGGCTG	AGCGCTG	AGACTG	1527	
QY	401	GI	ValArgLeu	SerPro	ArgAla	TrpThrAla	ProProAla	CysGlnPro	ProMetGluPro	420
Db	1528	GGCGGCTTTCC	CAAGCTTCA	CGGCCCCA	CTGCTG	CCAGCA	CCCATG	AGACT	1587	
QY	421	GI	UAsnLeu	AsnLysGlnSer	ProThrLys	LeuSerAla	SerGlyLys	AspSerThrIle	440	
Db	1588	GAGAACCTTG	ACCTCCAGTCC	CCCAACAG	CTGAGTCC	AGCGGGAG	AGACTCCAC	CAATC	1647	
QY	441	Pro	GlnAla	SerAsnArgLeu	AsnAlaIle	ValAsnArg	SerMetThr	LysSerPro	ArgSer	460
Db	1648	CCAAAGCCAG	CGCGGCTCTCA	TAATATG	ATTAAAGTTC	AAAGTCA	AGAGGGCTCTCC	CCGCAAGC	1707	
QY	461	Se	SerSerGlu	SerHisSerPro	LysTrpMetHis	ProProLysCys	TrpSerCys	GlyLys	480	
Db	1708	AGCAGCGAG	AGCCACTCA	CACTTAATG	CAACCCCG	GAAGTCA	GTCTCGG	GGCTCT	1767	
QY	481	Gln	SerProGln	HisAlaGlu	MetCysLeu	HisThrAla	GlyPro	ThrPheAla	GluGlu	500
Db	1768	CAGTCCCA	CGACGATG	AGATGGCTT	CCACACCG	CTGGCCCC	AGGTTCC	GTGAGAGAG	1827	
QY	501	Met	GlyGlnThr	GlnSerGlu	TrpSerAsp	SerSerCys	GluAsnGlyAla	PhePheCys	520	
Db	1828	ATGGAGAG	AGCCCAAGTCT	GAATCTCA	GAATTCAGT	GTGAGAA	CGGGGCTTCTT	CTTCTGC	1887	
QY	521	Asn	GluCys	AspCys	ArgPhe	SerGluGln	AlaSerLeu	LysArgHis	ThrLeuGlnThr	540
Db	1888	AATGATG	TGACTGCGCTTCT	GTAGAGG	AGCTTCACT	CAAGAG	GCACACGCT	CTCAAGAC	1947	
QY	541	His	SerAspLys	ProTrpLys	CysAsnArg	CysGlnAla	SerPhe	ArgTrpLysGly	Asn	560
Db	1948	CACAGTGA	CAAACTTCA	MAATGAG	CCGCTG	CCAGGCTTCTT	CGGTAC	AAAGGCAAC	2007	
QY	561	Leu	AlaSerHis	LysTrpValHis	ThrGlyGlu	LysProTrp	ArgCys	AsnIleCys	Gly	580
Db	2008	CTCGCAG	CCCAAGACCTTCC	ATACCGGT	AGAAACCTTAT	CGTTGCA	ATCTG	AGACTG	CGG	2067
QY	581	Ala	GlnPhe	AsnArgPro	AlaAsnLeu	LysThrHis	ThrArgIleHis	SerGlyLys	600	
Db	2068	GCCCAAGT	CAACCGG	CCAGCACT	GTAAACCA	CTCAATTC	ACTTGG	AGAGAG	2127	
QY	601	Pro	TrpLysCys	GluThrCys	GlyAla	ArgPheValGln	ValAlaHis	LeuArgAlaHis	620	
Db	2128	CCCTTCA	AAATGGAACCTG	CGAGCCAG	ATTTGTAC	AGGTGG	CCCACTTCC	GTGCCAT	2187	
QY	621	Val	LeuIleHis	ThrGlyGlu	LysProTrp	CysGluIleCys	GlyThr	ArgPheArg	640	
Db	2188	GTGCTTAT	TCACACTG	TGAGAGG	CCATATCC	CTGTAATCTG	GGCACC	GGTTCCGG	2247	
QY	641	His	LeuGlnThr	LeuLysSerHis	LeuArgIleHis	ThrGlyGlu	LysProTrpHis	Gly	660	
Db	2248	CACCTTCA	GACTCTG	AAAGGCACTT	GTGAATCC	ACAAGAGAA	ACCTTAC	CAATGT	2307	

Oy	661	GIuNyCySaLeuNH; sPeARGH; iLySeRGI; nLeuArgLeuH; sLeuArgGI; nLyS	680
Db	2308	GAGAGGTACCTGCATTTCCGTACAAAGCCAGCTGCACATTCCTCGCCAGAG	2367
Oy	681	HiSgIyAlIaIeThRAnThrLySValGIaTyArgValSeRaIaThrAspLeuProPro	700
Db	2368	CATGGCCCATCACCACCAACCAAGTGCATATACCGCGGTGAGCCACTGACCTGCTCG	2427
Oy	701	GIuLeuProLySaIaCyS	706
Db	2428	GAGCTCCCAAGCTGC	2445
RESULT 6			
ADY19589			
ID	ADY19589	standard; DNA; 3536 BP.	
XX	AC		
XX	ADY19589;		
XX			
DT	05-MAY-2005	(first entry)	
XX			
DE	DNA encoding a PRO polypeptide, SEQ ID NO 5395.		
XX			
KW	Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;		
KW	Antirheumatic; Antiarthritic; Osteoporotic; Hemostatic; Antianemic;		
KW	Antithyroid; Antidiabetic; Nephrotropic; CNS-gen.; Hepatotropic;		
KW	Vitucide; Gastrointestinal-gen.; Antipsoriatic; Anticestatic;		
KW	Antiallergic; de; gene; diagnosis.		
XX			
OS	Homo sapiens.		
XX			
FN	WO2005016962-A2.		
XX			
PD	24-FEB-2005.		
XX			
PE	11-AUG-2004; 2004WO-US026249.		
XX			
PR	11-AUG-2003; 2003US-0493546P.		
XX			
PA	(GETH) GENENTECH INC.		
XX			
PI	Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;		
XX			
DR	WPI; 2005-182330/19.		
XX			
PT	New nucleic acid encoding PRO polypeptide, useful for diagnosing and		
PT	treating an immune related disorder, e.g. systemic lupus erythematosus,		
PT	rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.		
XX			
PS	Claim 1; SEQ ID NO 5395; 158bp; English.		
XX			
CC	The invention relates to an isolated nucleic acid encoding a PRO		
CC	polypeptide. The polypeptide, agonist or an antagonist, antibody,		
CC	composition, and method are useful for diagnosing and treating an immune		
CC	related disorder, e.g. systemic lupus erythematosus, rheumatoid		
CC	arthritis. The present sequence represents a PRO polypeptide.		
XX			
SEQ	Sequence 3536 BP; 936 A; 943 C; 835 G; 822 T; 0 U; 0 Other;		
Alignment Scores:			
Pred. No.:	1,4e-192	Length:	3536
Score:	3793.00	Matches:	706
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	14	Gaps:	0
US-10-755-889-18 (1-706) x ADY19589 (1-3536)			
Oy	1	MeTaLaSeRProAlaAspSerCySIlleGlnPheThrArgHISaIaSeRAspValLeuNH	20
Db	328	ATGGCTCGCCGCGTGAACAGCTGATTCAGTTCAACCGCCAGTGCAGATGATTTCTTCC	387
Oy	21	AsnLeuAaMArgLeuArgSerArgAspIleLeuThrAspValValIleValValSerArg	40

Db 388 AACCTTAATCGTCCGAGTGCAGACATCTTACGATGTTGTCTATTGTGTGAGCCCT 447
Qy 41 GUGInPheargAlaHislyrThrValLeuMetAlaCysSerGlyLeuPheYrSerIle 60
Db 448 GAGCATTTAAGAGCCCATAAACGGCTCTCATGCGCTGCGAGTGGCCGTCTTATACATC 507
Qy 61 PheThrAspGlnLeuLysCysAsnLeuSerValIleAsnLeuAspProGluIleAsnPro 80
Db 508 TTACAGACACGATTGAATGAAACCTTAGTGTATCAATCTAGATCTTGAGATCAACCT 567
Qy 81 GUGlYpHeCysAlleuLeuAspPheMetYrThrSerArgLeuAsnLeuArgGluGly 100
Db 568 GAGGATTTCTGATCTCTCGATTCATGTACATCTCGCTCAATTTGGGGAGGCG 627
Qy 101 AsnIleMetAlaValMetAlaThrAlaMetYrLeuGlnMetGluHisValValAspThr 120
Db 628 AACATCATGCTGTGTGTGTCACGGCTATGTACTCAGATGAGCATGTTGTGACACT 687
Qy 121 CysArgLysPheIleLysAlaSerGluAlaGlnMetValSerAlaIleLysProProArg 140
Db 688 TGCAGAAAGTTTATTAAAGCCAGTGAAGCAGAGATGTTTCTGCATCAAGCTCTCGT 747
Qy 141 GUGlYpHeLeuAsnSerArgMetLeuMetProGlnAspIleMetAlaYrArgGlyArg 160
Db 748 GAAAGATTCTCTCAACAGCCGGATGCTGATGCCCCAAGACATCATGCGCTATCGGGTCCG 807
Qy 161 GluValValGluAsnAsnLeuProLeuArgSerAlaProGlyCysGluSerArgAlaPhe 180
Db 808 GAGGTGTGTGAACAACCTGCACCTGAGAGAGCGCCCTGGTGTGAGCAAGCCCTT 867
Qy 181 AlaProSerLeuYrSerGlyLeuSerThrProAlaSerYrSerMetYrSerHis 200
Db 868 GCCCCAGCTGTACAGTGGCTGTGTCCACCGCCAGCTCTTATTCTCATGTACAGCCAC 927
Qy 201 LeuProValSerSerLeuLeuPheSerAspGluGluPheArgAspValArgMetProVal 220
Db 928 CTCCTGTGTACGAGCTCTCTCTCCGATGAGAGATTTGGGATGTCCGAGTGGCCGTGG 987
Qy 221 AlaAsnProPheProLysGluArgAlaLeuProCysAspSerAlaArgProValProGly 240
Db 988 GCCAACCCCTTCCCAAGAGCGCGGCACTCCCATGTAGTGTCCAGGCCACAGTCCCTGGT 1047
Qy 241 GluTyrSerArgProThrLeuGluValSerProAsnValCysHisSerAsnIleYrSer 260
Db 1048 GAGTACAGCCGCGGACCTTGTGAGGTGTCCCAATGTGTGCACAGCAATATCTATCA 1107
Qy 261 ProLysGluThrIleProGluGluAlaArgSerAspMetHisYrSerValAlaGluGly 280
Db 1108 CCCAAGGAAACATCCCAAGAGGCGACAGAGTGTATGTCACTACAGTGTGGCTGAGGCG 1167
Qy 281 LeuLysProAlaAlaProSerAlaArgAsnAlaProYrPheProCysAspLysAlaSer 300
Db 1168 CTCAAACTCTGCTGCTCCCTCAGCCCGAAATGCCCCCTCACTTCCCTGTGTCAAGGGCCAG 1227
Qy 301 LysGluGluGluValArgProSerSerGluAspGluIleAlaLeuHisPheGluProProAsn 320
Db 1228 AAAGAAAGAGAGACCTCTCTCGAAGATGAGATGCTCTGCAATTCGAGCCCAAT 1287
Qy 321 AlaProLeuAsnArgLysGlyLeuValSerProGlnSerProGlnLysSerAspCysGln 340
Db 1288 GCACCCCTGAACCGGAAGGCTGTGTATGTCCACAGAGCCCCCAAGAAATCTGACTGCGAG 1347
Qy 341 ProAsnSerProThrGluAlaCysSerSerLysAsnAlaCysIleLeuGlnAlaSerGly 360
Db 1348 CCCAACTCGCCCAAGAGGCTGTGCAGAGTAAAGATCTCGCATCTCCAGGCTTCTGCGC 1407
Qy 361 SerProProAlaLysSerProThrAspProLysAlaCysAsnTrpLysLysYrLysPhe 380
Db 1408 TCCCTTCACAGCAAGACCCCACTGACCCCAAGACCTGCAACTGGAAGAAATCAAGTTC 1467
Qy 381 IleValLeuAsnSerLeuAsnGlnAsnAlaLysProGlyGlyProGluGlnAlaGluLeu 400

Db 1468 ATGTGTCTCAACGCTTCAACCAAGATGCAACCAAGGAGGCGCTGAGAGGCTGAGCTG 1527
Qy 401 GYAArgLysSerProArgAlaThrThrAlaProProAlaCysGlnProProMetGluPro 420
Db 1528 GGGCGGCTTTTCCCAAGAGCTTACAGCGGCCCACTGCTGTGCACACCCATGAGGCT 1587
Qy 421 GluAsnLeuAspLeuGlnSerProThrLysLeuSerAlaSerGlyGluAspSerThrIle 440
Db 1588 GAGAACTTGACTTCAGATCCCAACCAAGCTGAGTGGCCAGCGGAGGAGCTCCACCATC 1647
Qy 441 ProGlnAlaSerArgLeuAsnAsnIleValAsnArgSerMetThrGlySerProArgSer 460
Db 1648 CCACAAAGCCAGCGGCTCAATACATCTGTAAACAGTCTCATACAGGCTCTCCCGCAGC 1707
Qy 461 SerSerGluSerHisSerProLeuYrMetHisProProLysCysThrSerCysGlySer 480
Db 1708 AGCAGAGAGGCACTCACCACTTACATGACACCCCGAATGTACAGTCTGCGGCTCT 1767
Qy 481 GlnSerProGlnHisAlaGluMetCysLeuHisThrAlaGlyProThrPheAlaGluGlu 500
Db 1768 CAGTCCCAACAGATGAGAGATGTGCTCCACACCGCTGGCCCAAGTTCGCTGAGAG 1827
Qy 501 MetGlyGluThrGlnSerGluTyrSerAspSerSerCysGluAsnGlyAlaPhePheCys 520
Db 1828 ATGGGAGAGACCAGCTGAGTACTCAGATTTCTAGCTGTGAGAAAGGGGCTTCTTTC 1887
Qy 521 AsnGluCysAspCysArgPheSerGluGluAlaSerLeuLysArgHisThrLeuGlnThr 540
Db 1888 AATGATGTGACTGGCGCTTCTGTGAGAGGCTCACTCAAGAGGACACGGCTGCAGACC 1947
Qy 541 HisSerAspLysProTyrLysCysAspArgCysGlnAlaSerPheArgTyrLysGlyAsn 560
Db 1948 CACAGTGAACAACTCAACAAGTGTACCGCTCCAGGCTCTCTCCGCTCAACAAGGCAAC 2007
Qy 561 LeuAlaSerHisLysThrValHisThrGlyGlyLysProTyrArgCysAsnIleCysGly 580
Db 2008 CTGCGCAGCCACAAGCCCTTCATACCGGTGAGAAACCTTATCGTTGCAACATCTGTGG 2067
Qy 581 AlaGlnPheAsnArgProAlaAsnLeuYrThrHisThrArgIleHisSerGlyGluLys 600
Db 2068 GCCAGTTCAACCGGCGACCACTGAAACCCACACTGAAATCACTGTGAGAGAAAG 2127
Qy 601 ProTyrLysCysGluThrCysGlyAlaArgPheValGlnValAlaHisLeuArgAlaHis 620
Db 2128 CCTCAAAATGCGAAACCTCGGAGCGCAGATTTGTACAGTGTGCCACCTCGTGCAT 2187
Qy 621 ValLeuIleHisThrGlyGlyLysProTyrProCysGluIleCysGlyThrArgPheArg 640
Db 2188 GTGCTTATCCACACTGTGTGAGAAAGCTTATCCTGTGAAATGTGTGGCACCGGTTCCGG 2247
Qy 641 HisLeuGlnThrLeuLysSerHisLeuArgIleHisThrGlyGluLysProTyrHisCys 660
Db 2248 CACCTTCAACCTGTGAAGCCACTGCGAATCCACACAGAGAGAAACCTTACATTTGT 2307
Qy 661 GluLysCysAsnLeuHisPheArgHisLysSerGlnLeuArgLeuHisLeuArgGlnLys 680
Db 2308 GAGAGTGTACTGATTCGATTCGTCACAAAGCAGCTGCACTTGGCGCGAAG 2367
Qy 681 HisGlyAlaIleThrAsnThrLysValGlnTyrArgValSerAlaThrAspLeuProPro 700
Db 2368 CATGGCGCATCACCAACCAAGGTGCAATACCGGTGTGAGCCACTGACGTGCTCCG 2427
Qy 701 GluLeuProLysAlaCys 706
Db 2428 GAGCTCCCAAGGCTGC 2445

RESULT 7
ADL82846
ID ADL82846 standard, cDNA; 3537 BP.
XX
AC ADL82846;
XX
DT 17-JUN-2004 (first entry)

XX Human PRO26296 cDNA, SEQ ID 48.
 XX
 XX Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;
 XX Antiallergic; Muscular; Neuroprotective; Nephrotoxic; Antiinflammatory;
 XX Gene Therapy; PRO: B cell related disorder; cancer;
 XX Immune-mediated inflammatory disease; human; gene; ss.
 XX
 XX Homo sapiens.
 XX
 XX MO2004024097-A2.
 XX
 XX 25-MAR-2004.
 XX
 XX 15-SEP-2003; 2003MO-US029097.
 XX
 XX 16-SEP-2002; 2002US-0411392P.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI,
 XX Wu TD;
 XX
 XX WPI; 2004-329389/30.
 XX
 XX P-PSDB; ADL82847.
 XX
 XX New PRO polypeptide, useful for diagnosing and treating a B cell related
 XX disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune
 XX mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.
 XX
 XX Claim 2; Fig 48; 695pp; English.
 XX
 XX The present invention relates to PRO proteins and their coding sequences.
 XX The PRO proteins are useful for diagnosing and treating a B cell related
 XX disorder, e.g. X-linked infantile hypogammaglobulinemia, polyasccharide
 XX antigen unresponsiveness, selective IgA deficiency, selective IgM
 XX deficiency, selective deficiency of IgG subclasses, immunodeficiency with
 XX hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's
 XX lymphoma, intermediate lymphoma, follicular lymphoma, type II
 XX hyperendemicity, rheumatoid arthritis, autoimmune mediated haemolytic
 XX anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or
 XX ankylosing spondylitis. The PRO proteins are also useful for preparing a
 XX medicament for treating a condition that is responsive to the PRO
 XX protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO
 XX coding sequences are useful as hybridization probes in chromosome and
 XX gene mapping, in preparing PRO proteins, or in generating transgenic
 XX animals or knockout animals, which in turn are useful in the development
 XX and screening of therapeutically useful reagents.
 XX
 XX SQ Sequence 3537 BP; 940 A; 939 C; 832 G; 826 T; 0 U; 0 Other;
 XX
 XX Alignment Scores:
 XX Pred. No.: 9.94e-192 Length: 3537
 XX Score: 3777.00 Matches: 703
 XX Percent Similarity: 99.7% Conservative: 1
 XX Best Local Similarity: 99.6% Mismatches: 2
 XX Query Match: 99.6% Indels: 0
 XX DB: 12 Gaps: 0
 XX
 XX US-10-755-889-18 (1-706) x ADL82846 (1-3537)
 QY 1 MetaLaserProAlaSerProAlaSerCysAlaGlnPheThrArgHisAlaSerAspValLeuLeu 20
 DB 328 ATGGCTCTGCGCGGCTGACAGCTGATTCAGTTCAACCGCCATGCGAGAGTCTTCTTC 387
 QY 21 AsnLeuAsnArgLeuArgSerArgAspLleLeuThrAspValValIleValIleSerArg 40
 DB 388 AACCTTAATCGTCTCCGAGAGTCGAGACATCTGACTGATGTGTCAATGTGTGAGCGGT 447
 QY 41 GlnGlnPheArgAlaHisAlaValThrValLeuMetAlaCysSerGlyLeuPheTyrSerIle 60
 DB 448 GAGCAGTTAAGAGCCCATTAACCGGTCTTCATGCGCTCGCATGAGCTTCTTATAGCATC 507

QY 61 PheThrAspGlnLeuLeuCysAsnLeuSerValIleAsnLeuAspProGlnIleAsnPro 80
 DB 508 TTTACAGACCAAGTTGAATGAACCTTATGTGTATCATCAATCTAGATCCAGATCAACCTT 567
 QY 81 GlnGlyPheCysAlleLeuLeuAspPheMetTyrThrSerArgLeuAsnLeuArgGlnGly 100
 DB 568 GAGGAGTTCTGCAATCTCTCCGACTTCATGTACACATCTCGGCTCAATTTGCGGAGGGC 627
 QY 101 AsnIleMetAlaValMetAlaThrAlaMetTyrLeuGlnMetGlnHisValIleAspThr 120
 DB 628 AACATCATGCTGTGTATGCGACGCTATGTATCTCAATGAGAGATGTTGTGACACT 687
 QY 121 CysArgLysPheIleLeuValAsnSerGlnAlaGlnMetValSerAlaIleLysProProArg 140
 DB 688 TGCCGAAAGTTTATTAAGCCAGTGAAGAGATATGTTTCTCCATCAAGCCCTCGT 747
 QY 141 GlnGlnPheLeuAsnSerArgMetLeuMetProGlnAspLleMetAlaTyrArgGlyArg 160
 DB 748 GAAAGATTCCTCAACAGCCGAGATGTATGCCCCCAAGACATCATGCGCTATCGGGCTCGT 807
 QY 161 GluValValGlnAsnAsnLeuProLeuArgSerAlaProGlyCysGlnSerArgAlaPhe 180
 DB 808 GAGGTGTGAGAAACAACCTGCATGAGAGAGGCCCTGTGTGTAGACCAAGCTT 867
 QY 181 AlaProSerLeuTyrSerGlyLeuSerThrProProAlaSerTyrSerMetTyrSerHis 200
 DB 868 GCCCAAGCTGTACAGTGGCTGTGTCAACCCGCAACCTTATTCATGACAGCAC 927
 QY 201 LeuProValSerSerLeuLeuPheSerAspGlnGlnPheArgAspValArgMetProVal 220
 DB 928 CTCCTGTGACGAGCCCTCTCTTCGATGAGAGATTTGGGATGTCGGAATGCCGTGTG 987
 QY 221 AlaAsnProPheProLysGlnAlaValAlaLeuProCysAspSerAlaArgProValProGly 240
 DB 988 GCCAACCCTTCCCAAGAGCGGCACTCCATGTATGTATGTCAGAGCCAGTCCCTGTGT 1047
 QY 241 GlnTyrSerArgProThrLeuGlnValSerProAsnValCysHisSerAsnIleTyrSer 260
 DB 1048 GAGTACAGCGCGGCGAGCTTGTGAGGTGTCCCAATGTGTGCCACAGCATATCTATTTCA 1107
 QY 261 ProLysGlnThrIleProGlnGlnAlaArgSerAspMetHisTyrSerValAlaGlnGly 280
 DB 1108 CCCAAGAAACATCCCAAGAGAGGACGAGATATGACATCACTATGCTGAGAGGC 1167
 QY 281 LeuLysProAlaAlaProSerAlaArgAsnAlaProTyrPheProCysAspLysAlaSer 300
 DB 1168 CTCAACCTGCTGCGCCCTCAGCCGAAATGCCCTTACTTCTGTGTGACAGGCCAGC 1227
 QY 301 LysGlnGlnGlnArgProSerSerGlnAspGlnIleAlaLeuHisPheGlnProProAsn 320
 DB 1228 AAAGAAAGAGAGAACCTCTCGAAGATGATGATTCCTGCAATTCAGACCCCCCAAT 1287
 QY 321 AlaProLeuAsnArgLysGlyLeuValSerProGlnSerProGlnLysSerAspCysGln 340
 DB 1288 GCACCCCTGAACCGAAGGCTGTGTATGTGTACAGAGCCCCCAAGAAATCGATGACGAG 1347
 QY 341 ProAsnSerProThrGlnAlaCysSerSerLysAsnAlaCysIleLeuGlnAlaSerGly 360
 DB 1348 CCCAATCTGCGCCACAGAGTCTGTGACAGTAAATCTCTGACATCTTCAGGCTTCTGGC 1407
 QY 361 SerProProAlaLysSerProThrAspProLysAlaCysAsnTyrLysValPhe 380
 DB 1408 TCCCTCTCAGCAAGAGCCCACTGACCCCAAGACCTGCAACGTGAAGAAATACAAAGTTC 1467
 QY 381 IleValLeuAsnSerLeuAsnGlnAsnAlaLysProGlyGlyProGlnGlnAlaGlnLeu 400
 DB 1468 ATCTGTCTCAACAGCTTCAACAGATGCCAATGCCAAGAGGGCTGTGAGCGCTGAGCTG 1527
 QY 401 GlyArgLeuSerProArgAlaTyrThrAlaProProAlaCysGlnProPheGlnPro 420
 DB 1528 GAGCGGCTTTCCCAAGAGCTTACACGCGCCCACTGCTGCGCAAGCCATATGAGGCT 1587
 QY 421 GluAsnLeuAspLeuGlnSerProThrLysLeuSerAlaSerGlyGlnAspSerThrIle 440

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Db      1588 GAGAACTTGACCTCCAGTCCCAACCAAGCTGAGTGCAGCGGGAGGACCTCCACATC 1647
Qy      441 ProGlnAlaSerArgLeuAsnAnll eValAsnArgSerMetThiGlySerProArgSer 460
Db      1648 CCACAAGCCAGCGGCTCATATACATCGTTAACAGGTTCATGACGGGCTCTCCGCCAGAC 1707
Qy      461 SerSerGlySerHisSerProLeuTyMeChisProProGlySerThiSerGlySer 480
Db      1708 AGCAGGAGAGCCATCCACCTTTCATGACACCCCGAAGTGCACGCTCTGGGCTCTT 1767
Qy      481 GlnSerProGlnHisAlaGluMetCysLeuHisThrAlaGlyProThrPheAlaGluGlu 500
Db      1768 CAGTCCCAACAGCATCAGAGATGTGCTCCACACCGCTGGGCCCGACGTTCCCTGAGGAG 1827
Qy      501 MetGlyGluThrGlnSerGluTySerSerPheSerSerCysGluAsnGlyAlaPhePheCys 520
Db      1828 ATGGGAGAGACCACAGCTGAGTACTCAGATTCTTACGCTGTGAGAACGGGGCTTCTTCTGC 1887
Qy      521 AsnGluCysAspCysArgPheSerGluGluAlaSerLeuLysArgHisThrLeuGlnThr 540
Db      1888 AATGAGTGTACTGCGCTTCTCTGAGAGAGGCTCTCAAGAGGCAACAGCTGCAAGCC 1947
Qy      541 HisSerAspLysProTyTrpLysCysAspArgCysGlnAlaSerPheArgTyTrpGlyAsn 560
Db      1948 CACAGTGAACAACCTTACAGATGTGACCGCTGCAGGGCTCTCCGCTTACAGAGGCAAC 2007
Qy      561 LeuAlaSerHisLysThrValHisThrGlyGluLysProTyArgCysAsnLysGly 580
Db      2008 CTGCGCAGCCACAAGACCGTCCATACCGGTGAGAAACCTTATCGTTGCAACATCTGTGGG 2067
Qy      581 AlaGlnPheAsnArgProAlaAsnLeuLysThrHisThrArgLysHisSerGlyGluLys 600
Db      2068 GCCCAGTTCACCGCGCAGCAACCTGAAACCCCACTGAAATTCATCTTGAGAGAGAG 2127
Qy      601 ProTyTrpLysCysGluThrCysGlyAlaArgPheValGlnValHisLeuArgAlaHis 620
Db      2128 CCTTACAAATGCGAAACCTGCGAGCGCAATTTGTACAGGTGGCCACCTCCGTGCCAT 2187
Qy      621 ValLeuLysHisThrGlyGluLysProTyProCysGluLysCysGlyThrArgPheArg 640
Db      2188 GTCTTATCCACACTGGTGTGAGAAACCTTATCCCTGTGAAATCTGTGGCACCCGTTCCGG 2247
Qy      641 HisLeuGlnThrLysSerSerHisLeuArgLysHisThrGlyGluLysProTyTrpHisCys 660
Db      2248 CACCTTCAGACTGTGAGAGCCACCTGCGAATCCACACAGAGAGAAACCTTACCAATGT 2307
Qy      661 GluLysCysAsnLeuHisPheArgHisLysSerGlnLeuArgLeuHisLeuArgGlnLys 680
Db      2308 GAAAGGTAACTGCACTTCCGTCAAAAGCCAGCTGCGATTCATCTTGCCCGCAGAG 2367
Qy      681 HisGlyAlaLysThrAsnThrLysValGlnTyArgValSerAlaThrAspLeuProPro 700
Db      2368 CATGGCGGCATCAACCAACCAAGTGCATACCGCGTGCAGCACTGACCTGCGCTCCG 2427
Qy      701 GluLeuProLysAlaCys 706
Db      2428 GAGCTCCCAAGAGCTGC 2445

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RESULT 8
 ADY15005
 ID ADY15005 standard; DNA, 3630 BP.
 XX
 AC ADY15005;
 DT 05-MAY-2005 (first entry)
 XX
 DE DNA encoding a PRO polypeptide, SEQ ID NO 811.
 XX
 KW Antinflammatory; Immune disorder; Dermatological; Immunosuppressive;
 KW Antineumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;
 KW Antihypoid; Antidiabetic; Nephrotoxic; CNS-gen.; Hepatotropic;
 KW Virocide; Gastrointestinal-Gen.; Antiporiatic; Antiaesthetic;

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KW Antiallergic; ds; gene; diagnosis.
XX
OS Homo sapiens.
XX
PN WO2005016962-A2.
XX
PD 24-FEB-2005.
XX
PF 11-AUG-2004; 2004MO-US026249.
XX
PR 11-AUG-2003; 2003US-049346P.
XX
PA (GENTH) GENENTECH INC.
XX
PI Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;
XX
DR WPI; 2005-182330/19.
XX
PT New nucleic acid encoding PRO polypeptide, useful for diagnosing and
PT treating an immune related disorder, e.g. systemic lupus erythematosus,
PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.
XX
PS Claim 1; SEQ ID NO 811; 158bp; English.
XX
CC The invention relates to an isolated nucleic acid encoding a PRO
CC polypeptide. The polypeptide, agonist or an antagonist, antibody,
CC composition, and method are useful for diagnosing and treating an immune
CC related disorder, e.g. systemic lupus erythematosus, rheumatoid
CC arthritis. The present sequence represents a DNA encoding a PRO
XX polypeptide.
XX
SQ Sequence 3630 BP; 955 A; 959 C; 839 G; 877 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 1,02e-191 Length: 3630
Score: 3777.00 Matches: 703
Percent Similarity: 99.7% Conserves: 1
Best Local Similarity: 99.6% Mismatches: 2
Query Match: 99.6% Indels: 0
DB: 14 Gaps: 0
US-10-755-889-18 (1-706) x ADY15005 (1-3630)
Qy 1 MetAlaSerProAlaAspSerCysIleGlnPheThrArgHisAlaSerAspValLeu 20
Db 421 ATGGCTTCCCGGCTGACAGCTGTATCCAGTTCAACCCGCAAGCATGATGTTCTTCTC 480
Qy 21 AsnLeuAsnArgLeuArgSerArgAspIleLeuThrAspValValIleValAlaSerArg 40
Db 481 AACCTTAATCGTCTCCGAGTGCAGACATCTGACTGATGATGTGTGTTGTGAGACCGT 540
Qy 41 GluGlnPheArgAlaHisLysThrValIleMetAlaCysSerGlyLeuPheTySerIle 60
Db 541 GAGCATTTTAAAGCCCATTAACACGGTCCATAGGCTGTGAGGCGCTGTCTTATACATC 600
Qy 61 PheThrAspGlnLeuLysCysAsnLeuSerValIleAsnLeuAspProGluIleAsnPro 80
Db 601 TTACAGACCAAGTTGAATGCAACCTTAATGTGATTAATCTAGATCTAGATCAACCT 660
Qy 81 GluGlyPheCysIleLeuLeuAspPheMetTyTrpHisArgLeuAsnLeuArgGluGly 100
Db 661 GAGGATTTCTGACATCTCTGAGCTTCATGACATTCGAGTCAATTGGCGGAGAGGG 720
Qy 101 AsnIleMetAlaValMetAlaThrAlaMetTyTrpGlnMetGlnHisValAlaAspThr 120
Db 721 AACATCATGCTGTGTGATGTCACAGCGGTATGTACTTCACATGAGCATGTGTGACACT 780
Qy 121 CysArgLysPheLysLeuValAlaSerGluAlaGluMetValSerAlaLysProProArg 140
Db 781 TGCCGGAAGTTTATTAAGCCAGTGAAGCAGAGATGTTTCTGCCATCAAGCTCTCTGT 840
Qy 141 GluGlnPheLeuAsnSerArgMetCysLeuMetProGlnAspIleMetAlaTyArgGlyArg 160

```

Db 841 GAAAGATTCTCAACAGCGGATGCTGATGCCCAAGACATCATGCGCTATCGGGCT 900
 Qy 161 GUUValaGUUaAnuLeuProLeuArgSerAlaProGlyCySGluSerArgAlaPhe 180
 Db 901 GAGGTGTGAGAAACAACCTGACCTGAGAGAGCGCCCTGGTGTGAGACAGAGCCTT 960
 Qy 181 AlaProSerLeuTyrSerGlyLeuSerThrProProAlaSerTyrSerMetTyrSerHis 200
 Db 961 GCCCCAGCCTGTACAGTGGCTGTCCACACCGCCAGCCTCTTAATTCAGTACAGCAC 1020
 Qy 201 LeuProValSerSerLeuLeuPheSerAspGluGluPheArgAspValArgMetProVal 220
 Db 1021 CTCCCTGTGACAGCCTCTCTCTCTCCAGTACAGAGAGTTTGGAGTCCGAGTCCCTGTG 1080
 Qy 221 AlaAspProPheProLeuGluArgAlaLeuProCyAspSerAlaArgProValProGly 240
 Db 1081 GCCAACCCCTTCCCAAGAGAGCGGACCTCCCATGTATGTCAGAGCCAGTCCCTGT 1140
 Qy 241 GluTyrSerArgProThrLeuGluValSerProAsnValCySHisSerAsnIleTyrSer 260
 Db 1141 GAGTACAGCGCGCGCATTTGGAGTGTCCCCCATGTGTGCCACACCAATATCTATTCA 1200
 Qy 261 ProGlyGluThrIleProGluGluAlaArgSerAspMetHisTyrSerValAlaGluGly 280
 Db 1201 CCCAAGGAAACAATCCAGAGAGGACAGAGTATGCACTACAGTGTGGCTGAGAGGC 1260
 Qy 281 LeuLysProAlaAlaProSerAlaArgAsnAlaProTyrPheProCyAspLysAlaSer 300
 Db 1261 CTCAACCTGCTGCGCCCTCAGCGCCGAATGCCCTTACTTCCCTTGTGACAGAGCCAGC 1320
 Qy 301 LysGluGluGluArgProSerSerSerGluAspGluIleAlaLeuHisPheGluProProAsn 320
 Db 1321 AAAGAAGAAAGAGAGACCTCTCTCGAAGATGAGATTCCCTGCACTTTCAGAGCCCCCAAT 1380
 Qy 321 AlaProLeuAsnArgGlySerGlyLeuValSerProGluSerProGluLysSerAspCyGln 340
 Db 1381 GCACCCCTGAGACCGAAGGGGTGTGTTGTCACAGAGAGCCCCGAATATGACTGTGAG 1440
 Qy 341 ProAsnSerProThrGluAlaCySerSerTyrAsnAlaCySileuGluAlaSerGly 360
 Db 1441 CCCAATCGGCCCAAGAGTCTCTGACAGCATGTAAGATCTCTGCAAGCTTCTGGC 1500
 Qy 361 SerProProAlaLysSerProThrAspProLysAlaCyAsnTyrPlyLysPhe 380
 Db 1501 TCCCTCTCAGCCAGAGAGAGCCCACTGACCCCAACCTGCAACTGGAAGAAATACAAATTC 1560
 Qy 381 IleValLeuAsnSerLeuAsnGluAsnAlaLysProGlyGlyProGluGluAlaGluLeu 400
 Db 1561 ATCTGTCTCAACAGCTTCAACAGAAATGCCAAACAGAGGGGCTGAGAGGCTGAGCTG 1620
 Qy 401 GLyArgLeuSerProArgAlaTyrThrAlaProProAlaCySGlnProProMetGluPro 420
 Db 1621 GGCGCCCTTTCACAGAGCTTACAGCGCCCACTGCTGCTGACAGCCACCATGAGGCT 1680
 Qy 421 GluAsnLeuAspLeuGlnSerProThrLysLeuSerAlaSerGlyGluAspSerThrIle 440
 Db 1681 GAGAACTTGAACCTCCAGTCCCAACCAAGCTGAGTGCAGCGGAGAGAGATCCACACATC 1740
 Qy 441 ProGluAlaSerArgLeuAsnAsnIleValAsnArgSerMetThrGlySerProArgSer 460
 Db 1741 CCACAAAGCCAGCCGCTCAATACATGCTTAACAGTTCACAGAGGGGCTTCCCGCAGC 1800
 Qy 461 SerSerGluSerHisSerProLeuTyrMetHisProProLysCyThrSerCyGlySer 480
 Db 1801 AGCAGCGAGAGCCACTACCACTTACATGCAACCCCGGAAGTGCAGCTCTGCGGCTCT 1860
 Qy 481 GlnSerProGluHisAlaGluMetCysLeuHisThrAlaGlyProThrPheAlaGluGlu 500
 Db 1861 CAGTCCCAAGAGATGAGAGATGCTCCACACCGCTGAGCCCACTTCCCTGAGAGAG 1920
 Qy 501 MetGlyGluThrGlnSerGluTyrSerAspSerSerCySGluAsnGlyAlaPhePheCys 520
 Db 1921 ATGGAGAGACCAAGTCTGAGTACTCAGATTCTAGCTGTGAGAAAGGGGCTTCTTCTGCG 1980

Qy 521 AsnGluCysAspCyAspPheSerGluGluAlaSerLeuLysArgHisThrLeuGlnThr 540
 Db 1981 AATGAGTGTGACTGCGGCTTCTCTGAGAGGCTTCTCAAGAGGACACAGCTGCAAGAC 2040
 Qy 541 HisSerAspLysProTyrLysCyAspArgCySGlnAlaSerPheArgTyrLysGlyAsn 560
 Db 2041 CACGTGACAAACCTTACAAAGTGTACCGCTGCAAGGCTCTTCCGCTTACAGAGGCAAC 2100
 Qy 561 LeuAlaSerHisLysThrValHisThrGlyGluLysProTyrArgCyAsnIleCyGly 580
 Db 2101 CTGCGAGCCACAGAGCCCTTCCATACCGGTGAGAAACCCATATGTGCAACATCTGGG 2160
 Qy 581 AlaGlnPheAspArgProAlaAsnLeuLysThrHisThrArgIleHisSerGlyGluLys 600
 Db 2161 GCCAGATTCAACCGGCCAGCACTGAAACCCCAACCTCGAATTCATCTTGAGAGAGAG 2220
 Qy 601 ProTyrLysCySGluThrCySGlyAlaArgPheValAlaHisLeuArgAlaHis 620
 Db 2221 CCTTACAAATGCAAACTGCGAGCCAGATTTGTACAGTGGCCACCTCCGTGCCAT 2280
 Qy 621 ValLeuIleHisThrGlyGluLysProTyrProCySGluIleCySGlyThrArgPheArg 640
 Db 2281 GTGCTTATCCACACTGTGTAGAGAGCCCTATCCCTGTGAATCTGTGGACCCGTTCCGG 2340
 Qy 641 HisLeuGlnThrLeuLysSerHisLeuArgIleHisThrGlyGluLysProTyrHisCys 660
 Db 2341 CACCTTACAGCTCTGAGAGGCCACTGCGAATCCACAGAGAGAAACCTTACATTTGT 2400
 Qy 661 GluLysCyAsnLeuHisPheArgHisLysSerGlnLeuArgLeuHisLeuArgGluLys 680
 Db 2401 GAGAGGTGACCTGCACTTCTGTCACAAAGCCAGCTGCACTTCACTTGCAGAGAG 2460
 Qy 681 HisGlyAlaIleThrAsnThrLysValGlnTyrArgValSerAlaThrAspLeuProPro 700
 Db 2461 CATGGCGCATTCACCAACACCAAGTGCATATCCGGGTGCAAGCACTGACCTGCTCCG 2520
 Qy 701 GluLeuProLysAlaCys 706
 Db 2521 GAGCTCCCAAGAGCTGCG 2538

RESULT 9
 ADE53822/c
 ID ADE53822 standard; cDNA; 4506 BP.
 XX
 AC ADE53822;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human prostate cancer cDNA #169.
 XX
 KW Human; prostate cancer; ss; cDNA combination; differential expression;
 gene.
 XX
 OS Homo sapiens.
 XX
 PN US2003190640-A1.
 XX
 PD 09-OCT-2003.
 XX
 PF 29-MAY-2002; 2002US-00252157.
 XX
 PR 31-MAY-2001; 2001US-0295048P.
 XX
 PA (FARI/) FARIS M.
 PA (PEAR/) PEARSON C I.
 XX
 PI Faris M, Pearson CI;
 XX
 DR WPI; 2003-831619/77.
 XX
 PT New combination comprising cDNAs that are differentially expressed in
 prostate cancer, useful for diagnosing, treating or monitoring the

PT progression of treatment of prostate cancer.
XX
PS Claim 1, SEQ ID NO 169; 42pp; English.
XX
CC The invention relates to a combination comprising a number of cDNAs
CC expressed in prostate cancer. The invention also relates to a method for
CC detecting differential expression of one or more cDNAs in a sample
CC containing nucleic acids by hybridising a substrate with the nucleic
CC acids, thus forming one or more hybridisation complexes, detecting
CC hybridisation complex formation and comparing the complexes formed with
CC standard complexes, where differences between the standard and the sample
CC complex formation indicate differential expression of cDNAs in the
CC sample. The differential expression is diagnostic of prostate cancer. The
CC invention also relates to proteins and antibodies related to the cDNAs.
CC The combination is useful for diagnosing, treating or monitoring the
CC progression of treatment of prostate cancer. The antibodies are useful
CC for detecting prostate cancer. This sequence represents a human prostate
CC cancer cDNA of the invention.
XX
XX Sequence 4506 BP; 1113 A; 1102 C; 1135 G; 1156 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1,299-191 Length: 4506
Score: 3777.00 Matches: 703
Percent Similarity: 99.7% Conservative: 1
Best Local Similarity: 99.6% Mismatches: 2
Query Match: 99.6% Indels: 0
DB: 10 Gaps: 0
US-10-755-889-18 (1-706) x ADE53822 (1-4506)
QY 1 MetAlSerProAlaSerCysIleGlnPheThrArgHisAlaSerAapValLeuLeu 20
DB 3219 ATGACCTCGCGGCTGACAGCTGATTCACATTCACCCGACATCCAGTATGTTCTTCTC 3160
QY 21 AsnLeuAsnArgLeuArgSerArgAspIleLeuThrAspValIleValValSerArg 40
DB 3159 AACCTTATGCTGCTCCGGAATCGAGACATCTTACGATGTTGTCATTTGTTGAGCGGT 3100
QY 41 GlnGlnPheArgAlaHisIleValThrValLeuMetAlaCysSerGlyLeuPheTyrSerIle 60
DB 3099 GACGAGTTTGAAGCCCAATAAACGGTCTCATGGCCCGAGTGGCCCTGTTCTATAGCATC 3040
QY 61 PheThrAspGlnLeuLysCysAsnLeuSerValIleAsnLeuAspProGluIleAsnPro 80
DB 3039 TTATACAGACCAAGTGAATGCACACTTATGATGATCACTTACATCTCTGATCAGTACACCT 2980
QY 81 GlnGlyPheCysIleLeuLeuAspPheMetTyrThrSerArgLeuAsnLeuArgGlnGly 100
DB 2979 GAGGAGTTTGCATCCCTCGGACTTATGATACATCTCGGCTCAATTTGGCGGAGGCGC 2920
QY 101 AsnIleMetAlaValMetAlaThrAlaMetTyrLeuGlnMetGluHisValValAspThr 120
DB 2919 AACATCTATGCTGCTGATGAGCGCACCGCTATGATCTGATGAGTGTGTTGTGACACT 2860
QY 121 CysArgPhePheIleValAlaSerGlnAlaGluMetValSerAlaIleLysProProArg 140
DB 2859 TGGCGAAGTTTATTAAGGCCAGTAGAAGACAGATGTTTCTGCAATCAAGACCTCTCGT 2800
QY 141 GlnGlnPheLeuAsnSerArgMetLeuMetProGlnAspIleMetAlaTyrArgGlyArg 160
DB 2799 GAAAGATTCTCTCAACACCCGGAATCTGATGCCCAACATCATGCGCTATCGGGGCTGT 2740
QY 161 GluValValGluAsnLeuLeuProLeuArgSerAlaProGlyCysGluSerArgAlaPhe 180
DB 2739 GAGGTGTGTGAAGAACACTGCGCACTGAGAGCGCCCTGGGTGTGAGACAGAGCTTT 2680
QY 181 AlaProSerLeuTyrSerGlyLeuSerThrProProAlaSerTyrSerMetTyrSerHis 200
DB 2679 GCCCCAGGCTGTACAGTGGCTGTCTCCACCGCACCTCTTATTCACATGATACAGCAC 2620
QY 201 LeuProValSerSerLeuLeuPheSerAspGlnGlnPheArgAspValArgMetProVal 220

DB 2619 CTCCTGTACAGAGCTCTCTTCTCCGATGAGAGATTTCGGGATGCCGATGCTGTG 2560
QY 221 AlaAsnProPheProLysGluArgAlaLeuProCysAspSerAlaArgProValProGly 240
DB 2559 GCAACCCCTTCCCAAGAGAGCGGACCTCCCATGTATGATGCGAGCCAGTCCCTGGT 2500
QY 241 GlnTyrSerArgProThrLeuGlnValSerProAsnValCysHisSerAsnIleTyrSer 260
DB 2499 GAGTACAGCCGCGCATTTGGAGGTGTCCCCCATATGTGTGCACAGCAATATCTATTCA 2440
QY 261 ProLysGluThrIleProGlnGluValArgSerArgPheHisTyrSerValAlaGluGly 280
DB 2439 CCCAAGAAACATCTCCAGAAAGGACAGAAAGTATGACTACATGATGTGCTAGAGGC 2380
QY 281 LeuLysProAlaAlaProSerAlaArgAsnAlaProTyrPheProCysAspLysAlaSer 300
DB 2379 CTCGAACCTGCTGCCCCCTCAGCCGGAATGCCCCCTTACTTCTTGTGACAAAGCCAGC 2320
QY 301 LysGlnGlnGluArgProSerSerGlnLysAspGluIleAlaLeuHisPheGluProProAsn 320
DB 2319 AAAGAAAGAGAGACCTCTCCGGAAGTGAATTCCTGATTCGAGCCCCCAAT 2260
QY 321 AlaProLeuAsnArgLysGlyLeuValSerProGlnSerProGlnLysSerAspCysGln 340
DB 2259 GCACCCCTGAAACCGAAGGCTGTGTTAGTCCACAGAGCCCCCAGAAATCTGACTGCGAG 2200
QY 341 ProAsnSerProThrGlnAlaCysSerSerLysAsnAlaCysIleLeuGlnAlaSerGly 360
DB 2199 CCGAATCGCCACAGATCTCTGACAGATTAAGAAATGCTGTGATCTCCAGGCTTCTGGC 2140
QY 361 SerProProAlaLysSerProThrAspProLysAlaCysAsnTyrLysTyrLysPhe 380
DB 2139 TCCCCTCCAGCAAGAGCCCACTGACCCCAAGCCTGCACTGGAAGAAATACAAATTC 2080
QY 381 IleValLeuAsnSerLeuAsnGlnAsnAlaLysProProGlyProGlnGlnAlaGluLeu 400
DB 2079 ATCGTGTCTAAACAGCTCATAGATGCAAAACCAAGAGGAGCTGAGAGCTGAGCTG 2020
QY 401 GlyArgLeuSerProArgAlaTyrThrAlaProProAlaCysGlnProProMetGluPro 420
DB 2019 GGGCGCTTTCCTCCAGAGCTTACAGGCCCCCACTGCTGCGACGCCATCGAGCTT 1960
QY 421 GluAsnLeuAspLeuGlnSerProThrLysLeuSerAlaSerGlyGluAspSerThrIle 440
DB 1959 GAAACTTGACTTCAGTCCCAAGTCCCAACCAAGTGAAGTCCAGGGAGGACTCCACCATC 1900
QY 441 ProGlnAlaSerArgLeuAsnAsnIleValAsnArgSerMetThrGlySerProArgSer 460
DB 1899 CCAACAAGCCAGCGGCTCAATTAACATCGTTAACAGGTTCATGACGAGCTCTCCGCGAC 1840
QY 461 SerSerGluSerHisSerProLeuTyrMetHisProProLysCysThrSerCysGlySer 480
DB 1839 AGCAGGAGAGGCACTTACCACTTACATGACCCCCCAAGTGCACGTCTCGGCTCT 1780
QY 481 GlnSerProGlnHisAlaGluMetCysLeuHisThrAlaGlyProThrPheAlaGlnGlu 500
DB 1779 CAGTCCCAACAGATGACAGATGTGCTCCACACCGCTGCGCCCAAGTTCCTCGTAGAG 1720
QY 501 MetGlyGlnThrGlnSerGluTyrSerAspSerSerCysGluAsnGlyAlaPhePheCys 520
DB 1719 ATGGAGAGAACCCAGCTGATGATCTCAAGATTCTAGCTGTGAGAAACGGGCGCTTCTCTG 1660
QY 521 AsnGluCysAspCysArgPheSerGluGluAlaSerLeuLysArgHisThrLeuGlnThr 540
DB 1659 AATGATGTGACTGCGCTTCTCTGAGAGGCTCTCATAGAGGCAACAGCTGCAGACC 1600
QY 541 HisSerAspLysProTyrLysCysAspArgCysGlnAlaSerPheArgTyrLysGlyAsn 560
DB 1599 CACAGTGAACAACCTTACAAAGTGTACCGCTGCAGAGCCCTTCCTCGCTACAGAGCAAC 1540
QY 561 LeuAlaSerHisIleValHisThrGlyGlyLysProTyrArgCysAsnIleCysGly 580
DB 1539 CTCGACAGCCACAAAGACCGTCCATCCGGTGAAGAAACCTATGTGTGCAACATCTGTGG 1480

CC showed that the breakpoints on 3q27 were located within 3 kb of the same genomic locus, which was designated bcl-6. The human bcl-6 locus was identified by screening a phage cDNA library constructed from Bjab B-cell lymphoma mRNA. The sequence of an isolated clone is given in AA080513. CC bcl-6 is a proto-oncogene specifically involved in the pathogenesis of diffuse large cell lymphoma. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 3720 BP; 795 A; 902 C; 766 G; 696 T; 0 U; 561 Other;

Alignment Scores:

Pred. No.:	5,83e-191	Length:	3720
Score:	3763.00	Matches:	701
Percent Similarity:	99.4%	Conservative:	1
Best Local Similarity:	99.3%	Mismatches:	4
Query Match:	99.2%	Indels:	0
		Gaps:	0

US-10-755-889-18 (1-706) x AA080513 (1-3720)

QY 1 MetAlaSerProAlaAspSerCyAlleGlnPheThrArgHisAlaSerAspValIleuLeu 20
 Db ATGGCCCTCGCCGGCTGACAGTGTATCCAGTTACCCGCCATGCCAGGAGATTCTTCTC 387
 QY 21 AsnLeuAnArgLeuArgSerArgAspIleLeuThrAspValIleValValSerArg 40
 Db AACCTTATCGTCTCCGAGTGCAGACATCTTGACTGATGTTGTCATTTGTGTAGCCGT 447
 QY 41 GlnGlnPheArgHisIleValThrValIleuMetAlaCysSerGlyLeuPheTyrSerIle 60
 Db GAGAGATTGAGGCCATTAACGAGTCTCTCATGAGCTGGAGAGGCTGTGTTTATAGCATC 507
 QY 61 PheThrAspGlnLeuGlyCysAsnLeuSerValIleAsnLeuAspProGlnIleAsnPro 80
 Db TTTTACAGACAGTTGAATGCACTTATGTTGATCATCTAGATCCTGAGATCAACCT 567
 QY 81 GlnGlyPheCysIleLeuLeuAspPheMetTyrThrSerArgLeuAsnLeuArgGlnGly 100
 Db GAGGAGATTGTCATCTCTGACTTCATGTACATCTCGGCTCAATTTCGGGAGGAGC 627
 QY 101 AsnIleMetAlaValMetAlaThrAlaMetTyrLeuGlnMetGlnHisValValAspThr 120
 Db AACATCATGCTGTGATGAGCCACGAGCTATGTAAGCTGAGATGAGCATGTTGTGACACT 687
 QY 121 CysArgIysPheIleValAlaSerGlnAlaGlnMetValSerAlaIleValProProArg 140
 Db TGGCGAAGTTATTAAGCCAGTGAAGACAGATGTTTCTGCCATCAAGCTCTCTGT 747
 QY 141 GlnGlnPheLeuAnSerArgMetLeuMetProGlnAspIleMetAlaTyrArgGlyArg 160
 Db GAAAGGTTCTCAACAGCCGAGTGTATGCCCCAAGACATCATGCTTATCGGGGTCTGT 807
 QY 161 GlnValValGlnAsnAsnLeuProLeuArgSerAlaProGlyCysGlnSerArgAlaPhe 180
 Db GAGGTGGTGAAGAACATCTGCACTGAGAGCCCTCTGGGTGTGAAGAGAGAGCCCTT 867
 QY 181 AlaProSerLeuTyrSerGlyLeuSerThrProProAlaSerTyrSerMetTyrSerHis 200
 Db GCCCCACCTGTACAGTGGCTGTCCACACCGCAGCTCTTATTCATGTACAGCCAC 927
 QY 201 LeuProValSerSerLeuLeuPheSerAspGlnGlnPheArgAspValArgMetProVal 220
 Db CTCCTGTGACAGAGCTCTCTCTTCCGATGAGGATTTCGGGATGTCCGAGTGCCTGTG 987
 QY 221 AlaAsnProPheProGlyGlnArgAlaLeuProCysAspSerAlaArgProValProGly 240
 Db GCCAACCCCTTCCCAAGAGGCGGACATCCCATGTGATGTAGTCAGAGCCAGTCCCTG 1047
 QY 241 GlnTyrSerArgProThrLeuGlnValSerProAsnValCysHisSerAsnIleTyrSer 260
 Db GAGTACAGCCGCGCACTTTGAGGTGTCCCAATGTGTGACACAGCAATATCTATTTCA 1107
 QY 261 ProIysGlnThrIleProGlnGlnAlaArgSerAspMetHisTyrSerValAlaGlnGly 280

Db 1108 CCCAAGAAACATCCCAAGAGGCAAGAGATATGACTACAGTGTGGCTGAGGCG 1167
 QY 281 LeuLysProAlaAlaProSerAlaArgAsnAlaProTyrPheProCysAspValAlaSer 300
 Db CTCAAACCTGTGCCCCCTCAGCCCAAAATGCCCTTACTTCTTGTGTGCAAGGCGCAGC 1227
 QY 301 LysGlnGlnGlnArgProSerSerGlnAspGlnIleAlaLeuHisIlePheGlnProProAsn 320
 Db AAGAGAGAGAGAGACCTCTCTGAGAGATGATGATGCTTGCATTTCCAGCCCCCAT 1287
 QY 321 AlaProLeuAnArgIysGlyLeuValSerProGlnSerProGlnIysSerAspCysGln 340
 Db GCACCCCTGAACCGGAAGGCTGTGTTATGTCCACAGAGCCCAAGAAATCTGACTGCCAG 1347
 QY 341 ProAsnSerProThrGlnAlaCysSerSerLysAsnAlaCysIleLeuGlnAlaSerGly 360
 Db CCCAATCGCCCAAGAGGCTGTGACAGATGAATGCTTCATCTCCAGGGTTCGTGCG 1407
 QY 361 SerProProAlaLysSerProThrAspProLysValCysAsnThrLysTyrLysPhe 380
 Db TCCCTTCAGCCCAAGAGCCCACTGACCCCAAGCCCTGACGTGAGAGAAATACAACTTC 1467
 QY 1408 TCCCTTCAGCCCAAGAGCCCACTGACCCCAAGCCCTGACGTGAGAGAAATACAACTTC 1467
 QY 381 IleValLeuAnSerLeuAnGlnAsnAlaLysProGlyGlyProGlnGlnAlaGlnLeu 400
 Db ATGCTGTCAACAGCTTCAACAGATGCCAAACAGGGGGCTGAGCAGGCTGAGCTG 1527
 QY 1468 ATGCTGTCAACAGCTTCAACAGATGCCAAACAGGGGGCTGAGCAGGCTGAGCTG 1527
 QY 401 GlyArgLeuSerProArgAlaTyrThrAlaProProAlaCysGlnProPoweGlnPro 420
 Db GGCAGCTTTCCCAAGAGCTACAGGCTACAGGCCCCACCTGCGCAGCCACCATGAGACT 1587
 QY 1528 GGCAGCTTTCCCAAGAGCTACAGGCTACAGGCCCCACCTGCGCAGCCACCATGAGACT 1587
 QY 421 GlnAsnLeuAnPheGlnSerProThrLysLeuSerAlaSerGlyGlnAspSerThrIle 440
 Db GAGAACTTCACTTCAAGTCCCAACCAAGCTGAGTCCAGCGGAGAGACTCCACATC 1647
 QY 1588 GAGAACTTCACTTCAAGTCCCAACCAAGCTGAGTCCAGCGGAGAGACTCCACATC 1647
 QY 441 ProGlnAlaSerArgLeuAnAsnIleValAsnArgSerMetThrGlySerProArgSer 460
 Db CCAACAGCCAGCGGCTCAATTAACATGTATTAACAGTTCATGACGGCTCTCCCGCAGC 1707
 QY 1648 CCAACAGCCAGCGGCTCAATTAACATGTATTAACAGTTCATGACGGCTCTCCCGCAGC 1707
 QY 461 SerSerGlnSerHisSerProLeuTyrMetHisProProLysCysThrSerCysGlySer 480
 Db AGCAGCGAGAGCCACTCACTCACTTCACTCACTCCCGAAGTGCAGTCTCTGGGCTCT 1767
 QY 1708 AGCAGCGAGAGCCACTCACTCACTTCACTCACTCCCGAAGTGCAGTCTCTGGGCTCT 1767
 QY 481 GlnSerProGlnHisAlaGlnMetCysLeuHisThrAlaGlyProThrPheAlaGlnGln 500
 Db CAGTCCCAAGCAGTGAAGATGTGCTTCCACACCTGCGCCCAAGTTCGCTGAGAGAG 1827
 QY 1768 CAGTCCCAAGCAGTGAAGATGTGCTTCCACACCTGCGCCCAAGTTCGCTGAGAGAG 1827
 QY 501 MetGlyGlnThrGlnSerGlnTyrSerArgSerSerCysGlnAnGlnAlaPhePheCys 520
 Db ATGGAGAGAGCCAGTGTAGTACTCAAGTTCTAGCTGTGAGAACGGGCTTCTTCTGCG 1887
 QY 1828 ATGGAGAGAGCCAGTGTAGTACTCAAGTTCTAGCTGTGAGAACGGGCTTCTTCTGCG 1887
 QY 521 AsnGlnCysAspCysArgPheSerGlnGlnAlaSerLeuLysArgHisThrLeuGlnThr 540
 Db AATAGTGTACTGCGCTTCTCTGAGAGGCTTCACTCAAGAGGACACGCTGACAGCC 1947
 QY 1888 AATAGTGTACTGCGCTTCTCTGAGAGGCTTCACTCAAGAGGACACGCTGACAGCC 1947
 QY 541 HisSerAspLysProTyrLysCysAspArgCysGlnAlaSerPheArgTyrLysGlyAsn 560
 Db CACAGTCAAAACCTTCAAGTGTGACCGCTGCCAGGCTCTTCCCTCAAGAGGCAAC 2007
 QY 1948 CACAGTCAAAACCTTCAAGTGTGACCGCTGCCAGGCTCTTCCCTCAAGAGGCAAC 2007
 QY 561 LeuAlaSerHisIleValThrValHisThrGlnGlnLysProTyrArgCysAsnIleCysGly 580
 Db CTGCGCAGCCCAAGAGCTGTCAATACGGTGAAGAACCTTATGCTGACATCTGTGGG 2067
 QY 2008 CTGCGCAGCCCAAGAGCTGTCAATACGGTGAAGAACCTTATGCTGACATCTGTGGG 2067
 QY 581 AlaGlnPheAnArgProAlaAsnLeuLysThrHisThrArgIleHisSerGlyGlnLys 600
 Db GCCAAGTTCAACCGGCAAGCCCACTGAATAACCACTGAATTCATCTGAGAGAGAG 2127
 QY 2068 GCCAAGTTCAACCGGCAAGCCCACTGAATAACCACTGAATTCATCTGAGAGAGAG 2127
 QY 601 ProTyrLysCysGlnThrCysGlyAlaArgPheValGlnValAlaHisIleValArgAlaHis 620
 Db CCTTAAATGCGAAACCTGCGGAGCCAGATTTGTACAGGTGTGCCACCTCCGTCCTAT 2187
 QY 2128 CCTTAAATGCGAAACCTGCGGAGCCAGATTTGTACAGGTGTGCCACCTCCGTCCTAT 2187
 QY 621 ValIleuLysIleThrGlyGlnLysProTyrProCysGlnIleCysGlyThrArgPheArg 640

Db 2188 GTGCTTATGCAACGTGTGAGAAAGCCCTATCCCTGTGAATCTGTGACACCCGTTTCCGG 2247
 Qy 641 HtHleuGlnThleuLysSerHisleuAlaGllleHtHThGlyGluLysProGlyThrHisGys 660
 Db 2248 CACCTTCAGACTCTGAGAGGCCACTGCAATCCACAGAGAGAAACCTTACCACTTGT 2307
 Qy 661 GtLysCyAAsnuLeuHisPheArgHisLysSerGlnLeuArgLeuHisleuArgGlnLys 680
 Db 2308 GAGAGGTGTAACTGTGATTCCTGTCACAAAGCCACTGCGACTTCACTTGGCCCGAGAG 2367
 Qy 681 HtHglYAlaHleThraAnThLysValGlnTyArgValSerAlaThraPheLeuProPro 700
 Db 2368 CATGGGCGCATTCACCAACCAAGTGCATATCCGCGTGTCAAGCCACTGACCTGCTCCG 2427
 Qy 701 GtLysProLysAlaCys 706
 Db 2428 GAGCTCCCAAGCCTGC 2445
 RESULT 12
 ABI99745
 ID ABI99745 standard; cDNA; 2373 BP.
 AC ABI99745;
 XX 07-MAR-2002 (first entry)
 DT Mouse ischaemic condition related cDNA sequence SEQ ID NO:813.
 DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:813.
 XX Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
 KM vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.
 XX Mus musculus.
 OS
 XX WO200188188-A2.
 PN 22-NOV-2001.
 PD 18-MAY-2001; 2001WO-JP004192.
 PF 18-MAY-2000; 2000JP-00145977.
 PR (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
 PA Ishikawa K, Arai S, Takahashi Y, Nagata T, Ishii Y;
 XX IPI; 2002-034733/04.
 DR P-PSDB; ABB57289.
 DX Examining the ischemic condition (e.g. occlusive ischemia) by measuring
 PT expression levels of particular genes defined in the specification or by
 PT determining the expression profile of a gene group comprising these
 PT genes.
 XX Claim 2; Page 1999-2003; 2690BP; English.
 PS The present invention describes a method for examining ischemic
 XX conditions, comprising measuring the expression levels of particular
 CC genes (I) in a test sample or determining the expression profile of a
 CC gene group in the sample comprising genes selected from (I). The method
 CC is useful for examining the ischemic condition (e.g. compressive
 CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring the
 CC expression levels of particular genes (ABI99202 to ABI99912, encoding the
 CC protein sequences in ABB57020 to ABB57374) or by determining the
 CC expression profile of a gene group comprising these genes. The expression
 CC levels or expression profiles produced by these genes are used as an
 CC indicator when screening for ischemic condition-improving drugs or
 CC therapeutics for ischemic diseases. ABI9913 and ABI9914 represent PCR
 CC primers for a mouse ischaemic condition related sequence, which are used
 CC in the exemplification of the present invention
 XX Sequence 2373 BP; 566 A; 745 C; 574 G; 488 T; 0 U; 0 Other;
 SQ Alignment Scores:

Pred. No.:	1.24e-182	Length:	2373
Score:	3602.50	Matches:	666
Percent Similarity:	96.24	Mismatches:	14
Best Local Similarity:	94.28	Indels:	26
Query Match:	95.04	Gaps:	1
DB:	6		
US-10-755-889-18 (1-706) x ABI99745 (1-2373)			
Qy 1 MetAlaSerProAlaAspSerCysHlePheThraArgHisAlaSerAspValLeuLeu 20			
Db 101 ATGGCTCCCGCGCTGACAGCGTGAATCCAGTACCGCAAGTGAATGTTCTTC 160			
Qy 21 AenLeuAnaArgLeuArgSerArgAspHleuThraPheValHleValIserArg 40			
Db 161 AACCTTATCGCTCCGAGTGGGACATCTTGACGAGAGTTGTGATGATGGTGAAGCCGT 220			
Qy 41 GtLysPheArgAlaHisLysThraValLeuMetAlaCysSerGlyLeuPheTyrSerHle 60			
Db 221 GAGCAGTTTAGAGCCCATAGACAGTGCATAGCCTCAGCGGCTGTTCTTACAGTATC 280			
Qy 61 PheThraArgGlnLeuLysCysAsnLeuSerValHleAenLeuAspProGluHleAspPro 80			
Db 281 TTCACCTGACCAAGTGAATGCAACCTTGTATCAATCAATGATCTGAATTCAGCCCT 340			
Qy 81 GtLysPheCysHleLeuLysAspPheMetTyrThrSerArgLeuAsnLeuArgGluGly 100			
Db 341 GAGGCTTTTGCATCTCTCTGACATTCATGATCAATCTAGGCTCAACTGAGGGAAGCC 400			
Qy 101 AenHleMetAlaValMetAlaThraLametyTyrLeuGlnMetGluHisValIAspThr 120			
Db 401 AATATCATGGCGGTGATGACACAGCCATGTACCTGACATGAGATGTGTGTGACACA 460			
Qy 121 CysArgLysPheHleLysAlaSerGlnAlaGlnMetCysLysAlaHleLysProProArg 140			
Db 461 TCGAGAAATTATCATCAAGGCGCAGTGAAGCAAAATGGCCCTGACCTTAAACCTCCCGT 520			
Qy 141 GtLysPheLeuAsnSerArgMetLeuMetProGlnAspHleMetAlaTyrArgGlyArg 160			
Db 521 GAAAGTTCCTGAACAGCCGATGCTGATGCCCATGATCATATGAGCCATCCGAGGTGCT 580			
Qy 161 GtValAlaGluAsnAsnLeuProLeuArgSerAlaProGlyCysGluSerArgAlaPhe 180			
Db 581 GAGGTGTGAGAAACAATATGCCACTGAGAATAATCCCGGCTGTGAGAGAGAGCTTTT 640			
Qy 181 AlaProSerLeuTyrSerGlyLeuSerThrProProAlaSerTyrSerMetTyrSerHis 200			
Db 641 GCTCCCTCTGTATCAGTGGCTGTCAACACACAGCCCTTATCCCATGTACAGCCAT 700			
Qy 201 LeuProValSerSerLeuLeuPheSerAspGluGluPheArgAspVal---ArgMetPro 219			
Db 701 CTCCCGCTCAGACCTTCTCTCTCTGTATGAGAGCTCCGAGATGCCCCCGAATGCTT 760			
Qy 220 ValAlaAsnProPheProLysGluArgAlaLeuProCysAspSerAlaArgProValPro 239			
Db 761 GTGGCCAAACCTTTTCCCAAGAGAGCGTGCCTCCCTGCGAAGTCCGAGCAAGCTCCCT 820			
Qy 240 GlyGluTyrSerArgProThrLeuGlnValSerProAsnValCysHisSerAsnHleTyr 259			
Db 821 AATGATTAATAGACAGGCAACCATGAGGTGCCCAAGTTGTGTACAGCAACATCTAC 880			
Qy 260 SerProLysGluThrLeuProGluGluAlaArgSerAspMetHisTyrSerValAlaGlu 279			
Db 881 TCGCCCAAGAGAGCACTCCAGAGAGGCTCCGAGTACATACATCACTACAGTGGCTGAG 940			
Qy 280 GtLysLeuProAlaAlaProSerAlaArgAsnAlaProTyrPheProCysAspLysAla 299			
Db 941 GCGCCCAAGCTGTCTCTCTCTGCTCGGAATGCTCCATATCTCCCTGTGACAAAGCC 1000			
Qy 300 SerLysGluGluGluArgProSerSerGluAspGluHleAlaLeuHisPheGluProPro 319			
Db 1001 AGCAAGAAGAGAGAGACCTTCTTCTGAGAGATGAGATTTGCCCTGATTCGAGCCCCCT 1060			

QY 320 AsnAlaProLeuAenArglybGlyLeuValSerProGlnSerProGlnLysSerAspCys 339
 DB 1061 AATGACACCTTGAACCGAAGAGTCTGTTAGTCCCAAGTCCCGAATTCGACTGC 1120
 QY 340 GlnProAenSerProThrglnAlaCysSerSerLysAsnAlaCysIleLeuGlnAlaSer 359
 DB 1121 CAGCCCACTCAACCAAGAGTCTGCAAGCAAGCAAGCCTGCACTTCCAGGCTCT 1180
 QY 360 GlySerProProAlaLysSerProThrAspProLysAlaCysAsnTrpLysLeuTyrLys 379
 DB 1181 GGCTCTCGGACGCAAGAGCCCACTGACCCGAAGCTGCACTGGAAGAAATATAG 1240
 QY 380 PheIleValLeuAenSerLysAsnGlnAsnAlaLysProGlyGlyProGlnGlnAlaGlu 399
 DB 1241 TTCATCTCTTCAACAGCTCTCAATCAGAAATGCCAAACCGAGGCTCTGACAGAGCAGAG 1300
 QY 400 LeuAlaLysLeuSerProAlaLysTyrThrAlaProProAlaCysGlnProProMetGlu 419
 DB 1301 CTGGGTGGCTCTCCCTCGAGCTTACCTGCAACCGCCCTTGGCAGCCCTATGAG 1360
 QY 420 ProGlnAenLeuAenArgLysSerProThrLysLeuSerAlaSerGlyLysAspSerThr 439
 DB 1361 CCGCGAAGCTTGAATCTCACTCCCGCAAGCTCAAGTGCAGTGGGAGAGACTTACC 1420
 QY 440 IleProGlnAlaSerArgLeuAenAsnIleValAsnArgSerMetThrGlySerProArg 459
 DB 1421 ATCCCCCAAGCAGCCGGCTCAATATCTCTGAAACAGTCTCCGAGAGCTCCCGCCCA 1480
 QY 460 SerSerSerGlnSerLysSerProLeuTyrMetHisProProLysCysThrSerGly 479
 DB 1481 AGCAGCAGTGAAGTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 1540
 QY 480 SerGlnSerProGlnHisAlaGlnMetCysLeuHisThrAlaGlyProThrPheAlaGlu 499
 DB 1541 TCTCAGTCCCAAGCACTCAAGATGATGCTCCATATCTGCTGGGCCCAAGCTTCCCGAG 1600
 QY 500 GluMetGlyGlyIleThrglnSerGlyLysSerAspSerSerCysGluAsnGlyAlaPhe 519
 DB 1601 GAGATGGGGGAAACCACTCAAGATTAATTCGATTTCTACCTGTGAGAAAGGAGACCTTCTTC 1660
 QY 520 CysAsnGlnCysAspCysArgPheSerGlnGlnAlaSerLeuLysArgHisThrLeuGln 539
 DB 1661 TGCAACGATGTGATGCTGCTGTTCTCTGAGAGGCTGCTCAAGAGGCAACGCTGAG 1720
 QY 540 ThrHisSerAspLysProTyrLysCysAspArgCysGlnAlaSerPheArgTyrLysGly 559
 DB 1721 ACGCACTGACAAACCACTCAAAATGTATGCTGCCAGGCTCTTCCGCTACAAAGGC 1780
 QY 560 AsnLeuAlaSerHisLysThrValHisThrGlyLysProTyrArgCysAsnIleCys 579
 DB 1781 AACCTCGCAGCAAGCAAGACTGTCCACAGGGTGAGAAACCTATCGCTGTAACATTGT 1840
 QY 580 GlnAlaGlnPheAsnArgProAlaAsnLeuLysThrHisThrArgIleHisSerGlyLys 599
 DB 1841 GGAGGCGAGTTCAAATCGGCGAGCCCACTGAGAACCACTCGAATTCACCTGAGAAA 1900
 QY 600 LysProTyrLysCysGlnThrcysGlyAlaArgPheValGlnValAlaHisLysLeuArg 619
 DB 1901 AAGCCCTCAAAATGGAACCTGTGGGCGAGGTTGTTCAGGTGGCCCACTCCGTGCC 1960
 QY 620 HisValLeuIleHisThrGlyLysProTyrProCysGlnIleCysGlyThrArgPhe 639
 DB 1961 CACGTGCTCATTCACACTGAGAGAGAGCGTACCCCTGTGAATCTGTGGCAGCTGCTTC 2020
 QY 640 ArgHisLeuGlnThrcysLysSerHisLysValGlnIleHisThrGlyLysProTyrHis 659
 DB 2021 CGGCACTTCAAGACTCTGAGAGGCAATCGGCATTCACACAGAGAGAAACCTTACAT 2080
 QY 660 CysGlyLysCysAsnLeuHisPheArgHisLysSerGlnLeuArgLeuHisLysArgGln 679
 DB 2081 TGTGAAAGTGTAACTGCACTTGTCTCAAAAGCCAACTGCACTTGTGGCCAG 2140
 QY 680 LysHisGlyAlaIleThrAsnThrLysValGlnTyrArgValSerAlaThrAspLeuPro 699

DB 2141 AAGCAGCGGCGCATTCACAAACCAAGTCAATACGCTGTGGCGCTGACTGCTCT 2200
 QY 700 ProGlnLeuProLysAlaCys 706
 DB 2201 CCGAGCTCCCAAGCTTGC 2221
 RESULT 13
 ADEL13839
 ID ADEL13839 standard; DNA; 1440 BP.
 AC ADEL13839;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE AAC2-2 nucleotide sequence SEQ ID NO:2.
 XX
 KW carcinoembryonic antigen; CEA; CEA(6D)-1; 2; cytostatic; vaccine; cancer;
 KW tumour antigen; immunotherapy; angiogenesis-associated antigen; AAC2-2;
 KW gene; ds.
 OS Unidentified.
 OS
 PN WO2003085087-A2.
 XX
 PD 16-OCT-2003.
 XX
 PF 09-APR-2003; 2003WO-US010916.
 XX
 PR 09-APR-2002; 2002US-0372972P.
 XX
 PA (AVET) AVENTIS PASTEUR LTD.
 PA (THER-) THERION BIOLOGICS INC.
 PI Parrington M, Zhang L, Rovinski B, Griz LR, Greenhalgh T;
 XX
 DR WPI: 2003-877029/81.
 XX
 PT New isolated DNA molecule comprising the carcinoembryonic antigen (6D)-
 PT 1,2 sequence, useful for diagnosing, preventing and treating cancer, or
 PT determining the effectiveness of a chemotherapeutic or other treatment
 PT regimen.
 XX
 PS Disclosure; SEQ ID NO 2; 56bp; English.
 XX
 CC The present invention describes an isolated DNA molecule comprising the
 CC carcinoembryonic antigen (CEA) (6D)-1,2 sequence of 2106 bp (see
 CC ADEL13861), or its fragment. Also described: (1) an expression vector
 CC comprising the nucleic acid sequence CEA(6D)-1,2, or its fragment
 CC describing above; (2) a composition comprising the expression vector of
 CC (1) in a pharmaceutical carrier; and (3) preventing or treating cancer
 CC comprising administering to a host the expression vector of (1). CEA(6D)-
 CC 1,2 has cytostatic activity, and can be used in vaccines. The CEA(6D)-1,2
 CC nucleic acid and target polypeptide are useful for diagnosing, preventing
 CC and treating cancer, predicting prognosis, or determining the
 CC effectiveness of a chemotherapeutic or other treatment regimen. The
 CC expression vector may be used for the insertion and expression of CEA(6D)
 CC -1,2 nucleic acid encoding tumour antigens for the immunotherapeutic
 CC treatment of cancer. The target polypeptides are useful in generating
 CC antibodies used in screening assays or for immunotherapy. The present
 CC sequence represents the angiogenesis-associated antigen AAC2-2, which is
 CC given in the exemplification of the present invention.
 XX
 SO Sequence 1440 BP; 300 A; 503 C; 381 G; 256 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.21e-52 Length: 1440
 Score: 1155.00 Matches: 268
 Percent Similarity: 46.6% Conservative: 58
 Best Local Similarity: 38.3% Mismatches: 142
 Query Match: 30.5% Indels: 232
 DB: 10 Gaps: 15

US-10-755-889-18 (1-706) x ADEI3839 (1-1440)

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QY 1 MetAlaSerProIa-----AspSerCysIle-----GlnPheThrArgHis 14
Db 1 ATGGATTCCCGCCCGCCCGAGGAGGCGCTGGAGTCCGACGATTCACCTCCCGAC 60
QY 15 AlaSerAspValIleuLeuAenLeuAenArgLeuArgSerArgAspIleLeuThrArgVal 34
Db 61 TCTCCGACGCTGCTGGGCAACCTCAACGACGCTGCTGGCGGAGATCCCTCACTGACGTC 120
QY 35 ValIleValIaSerArgGlnGlnPheArgAlaHisIleYThrValIleuMetAlaCysSer 54
Db 121 ACCCTGCTGGTGGCGGCAACCCCTCAGACGACACAGGCAAGTTCATCGCTCAGAT 180
QY 55 GlyLeuPheThrSerIlePheThrArgGlnLeuIleCysAsnLeuSerValIleAsnLeu 74
Db 181 GGGCTTCTTATTCATTTTCGGGGCGCTGGCGGAGTCCGGGTGGAACGTCCTCTCTG 240
QY 75 AspProGluIleAsnProGluGlnIlePheCysIleLeuLeuAspPheMetIleThrSerArg 94
Db 241 CCGGGGGGTCGCCAAGCGAGAGGCTTCGCCCCCTTATTTGACTTCATGTAACACTTCGCGC 300
QY 95 LeuAsnLeuArgGlnGlnIleMetAlaValMetAlaThrAlaMetIleGlnMet 114
Db 301 CTGGGCTCTCTCCAGCCACTGCACCGACGAGTCTTACGGCGCCCACTATTTCAGAGATG 360
QY 115 GlnHisValIaIlePheThrCysArgIlePheIleValIaSerGlnIaGlnMetValSer 134
Db 361 GAGCAGCTGGTCCAGGCGATGCCACCGCTTCATCCAGGCCAGC----- 402
QY 135 AlaIleYAspProArgGlnGlnIlePheLeuAsnSerArgMetLeuMetProGlnAspIle 154
Db 402 ----- 402
QY 155 MetAlaIleArgGlnIaGlnValIaGlnAsnAsnLeuProLeuArgSerAlaProGln 174
Db 402 ----- 402
QY 175 CysGlnSerArgAlaPheAlaProSerLeuIleYSerGlnLeuSerThrProProAlaSer 194
Db 402 ----- 402
QY 195 TyrSerMetIleYSerHisLeuProValIleSerSerLeuPheSerAspGlnIlePheArg 214
Db 403 -----TATGAACCTCTGGGCGATCTCC----- 423
QY 215 AspValaIleArgMetProValaIaAsnProPheProIleGlnIaGlnIaLeuProCysAspSer 234
Db 423 ----- 423
QY 235 AlaArgProValaIleProGlnGlnIleYSerArgProThrLeuGlnValIleSerProAsnValaCys 254
Db 423 ----- 423
QY 255 HisSerAsnIleYSerProIleYSerGlnIleThrIleProGlnGlnIaIaArgSerAspMetHis 274
Db 423 ----- 423
QY 275 TyrSerValaIaGlnGlnIleuYAspProAlaIaIaProSerAlaIaArgAsnAlaProIleYrPhe 294
Db 424 -----CTGGCGCCCTG----- 435
QY 295 ProCysAspIleYAspIleYSerGlnIleGlnIleArgProSerSerGlnIleAspGlnIleAlaLeu 314
Db 436 -----GAAGCAGAACCCCAACA----- 453
QY 315 HisPheGlnProProAsnAlaProLeuAsnArgIleYSerGlnValIleSerProGlnIleSerPro 334
Db 454 -----CCCCCAAGGCGCT----- 483
QY 335 GlnIleYSerAspCysGlnProAsnSerProThrGlnIaCysSerSerIleYAsnAlaCys 354
Db 484 AGGCGCTCCGAGAGACCCAGACCCAGCTTAATCTGAATCTGAGAC----- 528
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QY 355 IleLeuGlnAlaSerGlySerProProAlaIleYSerSerProThrAspProIleYAsnValaCysAsn 374
Db 529 -----TGCAAGTCAGAGGCGCCCGCCAGCTCCAGGACGCGTCCAGACCCAGGCGCTGCAGAC 579
QY 375 TrpIleYSerYrIleYAspIleValaIleuAsnSerLeuAsnGlnAsnAlaIleYProGlnGly 394
Db 580 TGGAAAAGTACAAATACATCGCTTAAATCTCT----- 612
QY 395 ProGlnGlnAlaGlnLeuGlnIleYArgLeuSerProArgAlaIleYThrAlaProProAlaCys 414
Db 613 ---CAGGCTCCCAAGCAGGAGCGCTGCTGGGAGAGAGAGTTCGTGTAACCTTGCCCGC 669
QY 415 GlnProProMetGlnProGlnIleuAsnLeuAspLeuGlnIleSerProThrIleYLeuSerAlaSer 434
Db 670 CAAGCAGGCTCCCGACGTGAGACGAGGCTCCAGCAGAGACGACGACGACGACGACGAC 729
QY 435 GlnIleAspSerThrIlePro---GlnAlaSerArgLeuAsnAsnIleValaIleAsnArgSer 453
Db 730 AGTGAAGAAGAACCACTTCCTGTCGCCAGACGAGCTC----- 768
QY 454 MetIleGlnYSerProArgSerSerSerGlnIleSerHisSerProLeuIleYrMetHisProPro 473
Db 769 -----TCTCCAAGTGTCTGCACGTGCAGTTC----- 795
QY 474 IYsCysThrSerCysGlnSerGlnSerProGlnHisAlaGlnMetCysLeuHisIleThrAla 493
Db 796 -----AAATGTGG-----GCTCCAGCAGATGACCCCTACCTCTCCATCTCCAG 840
QY 494 GlnProThrPheAlaGlnIleuMetGlnIleGlnIleGlnIleYSerArgSerSerCys 513
Db 841 -----GCTCAAGACACTTCGTGATCACTTCGTAACGAGGCTGTGTCACACTACCG 888
QY 514 GlnAsnGlnAlaPhePheCysAsnGlnIleYAspProYrArgPheSerGlnIleIleSerLeu 533
Db 889 GGAAGTAATTTTACGCTGCGAGAACTGTGAGCTGTGAGCTGCGAGGCTCTCATCTGGAGGCTG 948
QY 534 IYsArgHisIleThrLeuGlnIleThrHisSerAspIleYrProIleYrCysAspArgCysGlnAla 553
Db 949 GAC---TCCTTGCTTCTCTGGAGCAGACGAACTGTAAGTGTACGCTGTGCGGTCT 1005
QY 554 SerPheArgIleYrGlnIleuAsnIleSerHisIleYrThrValHisIleThrGlnIleYrPro 573
Db 1006 TCGTTCGCTTACAGGCGAACCTTGGCAGTCACTGTAAGTGTACGCTGTGCGGTCT 1065
QY 574 TyrArgCysAsnIleYrGlnIleuAsnIleGlnIlePheAsnArgProAlaIleuIleYrThrHis 593
Db 1066 TACCACTGCTCAATCTGCGAGCGCTTTTAACTGGCAGCAAACTGTAAGACGACAGC 1125
QY 594 ArgIleHisSerGlnIleYrProIleYrCysGlnIleThrCysGlnAlaIaArgPheValaGln 613
Db 1126 CGCATCAATTCGGAGAGAGAACCGCTTAAGTGTGAGACCTGCGGCTTGTGTAACAG 1185
QY 614 ValAlaHisLeuArgAlaHisIleValIleuIleHisIleThrGlnIleYrProIleYrProCysGln 633
Db 1186 GTGGCAGATCTGGGCGGCGACGCTGATCCACACCGGAGAGAACCTTACCTTGCCCT 1245
QY 634 IleCysGlnIleYrArgPheArgHisIleuGlnIleThrIleYrSerHisIleuArgIleHisIleThr 653
Db 1246 ACCCTGGAGAACCGCTTCCGCCACTGCAGACCTTCMAAGCCACCTTGACATCCACACC 1305
QY 654 GlnIleYrProIleYrHisIleCysGlnIleYrCysAsnIleuHisIlePheArgHisIleYrSerGlnIle 673
Db 1306 GAGAGAGAGCTTACATCTGAGACCCCTGTGCTGATCTCCGAGCAAGAGTCAACTG 1365
QY 674 ArgLeuHisLeuArgGlnIleYrHisIleGlnIleYrAsnIleYrValaGlnIleYrArgVala 693
Db 1366 CGGCTGATCTGGCGAGAAACCGAGCTGTACCAACCAAGTGTACATCCACAT 1425
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RESULT 14

AAL56278

ID AAL56278 standard; DNA; 1440 BP.

XX

AC AAL56278;
 XX 11-MAR-2004 (first entry)
 DT AAC2-2 open reading frame.
 DE
 XX Angiogenesis; cancer; AAC2-1; AAC2-2; tumour antigen; expression vector;
 KW cytosolic; gene therapy; gene; ds.
 XX Unidentified.
 OS
 PN MO2003080800-A2.
 XX
 PD 02-OCT-2003.
 XX
 PF 20-MAR-2003; 2003WO-US008536.
 XX
 PR 20-MAR-2002; 2002US-0365982P.
 XX
 XX (AVET) AVENTIS PASTEUR INC.
 XX
 XX Berrinstein N, Lovitt C, Farrington M, Pedyczak A, Radvanyi L,
 PI Singh-Sandhu D;
 XX WPI; 2003-779251/73.
 DR P-PSDB; AB064323.
 XX
 XX New expression vector for preventing or treating an angiogenesis-
 PT dependent disease (e.g. breast cancer) comprises a nucleic acid sequence
 PT that encodes the angiogenesis-associated antigen AAC2-1 or AAC2-2.
 XX
 XX Claim 54; Page 57; 57pp; English.
 XX
 XX The present invention relates to an expression vector for inducing an
 CC anti-tumour immune response in a patient. Also provided is a method of
 CC using such a vector to treat angiogenesis-dependent diseases. The
 CC composition and methods are useful in diagnosing, preventing, prognosing
 CC or treating an angiogenesis-dependent disease, preferably a breast
 CC cancer. The DNA molecule and protein may also be used in drug screening
 CC assays. The present sequence is an AAC2 coding sequence shown in the
 CC exemplification of the invention
 CC
 XX
 SQ Sequence 1440 BP; 300 A; 503 C; 381 G; 256 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1,21e-52 Length: 1440
 Score: 1155.00 Matches: 268
 Percent Similarity: 46.6% Conservative: 58
 Best Local Similarity: 38.3% Mismatches: 142
 Query Match: 30.5% Indels: 232
 DB: 10 Gaps: 15
 US-10-755-889-18 (1-706) x AAL56278 (1-1440)
 QY 1 MetAlaSerProAla-----AspSerCysIle-----GlnPheThrArgHis 14
 DB 1 ATGGGTTCCCGCCCGCCGAGGAGCGCTGCGGCTACGTCCGGAATTCACTCGCCAC 60
 QY 15 AlaSerAspValIleuLeuAsnLeuAsnArgLeuArgSerArgAspIleLeuThrAspVal 34
 DB 61 TCCTCCGACGTGCTGGGCACTCAACGAGCTGCGCTCGCGGAGTCTCACTGACGTC 120
 QY 35 ValIleValIleSerArgGluGlnPheArgAlaHisIstYrThrValIleuMetAlaCysSer 54
 DB 121 ACGCTGCTGTGGGGGCAACCCCTCAGAGACACCAAGGCACTTCTATCGCCGCACT 180
 QY 55 GlysLeuPheIleYrSerIlePheThrAspGlnLeuIleuIleuIleuIleuIleu 74
 DB 181 GGGTCTCTCTATTCATTTTCGCGGCGCGTGGGAGTGGGAGTGGAGCTGCTCTCTG 240
 QY 75 AspProGluIleAsnProGluIlePheCysIleLeuLeuAspPheMetCysThrSerArg 94
 DB 241 CCGCGGGGTCCCGAAGCAGAGAGCTTCCCTCTATTGACACTGATCACTTCGCGC 300

QY 95 LeuAsnLeuArgGluGluValAsnIleMetAlaValMetAlaThrAlaMetCysLeuGlnMet 114
 DB 301 CTGCGCTCTCTCCACCGACCTGCAACGAGTCTTCAGCGCCGACCTATTTCGACATG 360
 QY 115 GlnHisValValAspThrCysArgIlePheIleValAlaSerGluIleGluMetValSer 134
 DB 361 GAGCAGCTGTGTCAGGAGCATGCCACCGCTTCACTCAGCGCCAGC----- 402
 QY 135 AlaIleLeuProAlaArgGluGluPheLeuAsnSerArgMetLeuMetProGlnAspIle 154
 DB 402 ----- 402
 QY 155 MetAlaTyrArgGlyArgGluValValGluAsnAsnLeuProLeuArgSerAlaProGly 174
 DB 402 ----- 402
 QY 175 CysGluSerArgAlaPheAlaProSerLeuTyrSerGlyLeuSerThrProProAlaSer 194
 DB 402 ----- 402
 QY 195 TyrSerMetCysIlePheProValSerSerLeuLeuPheSerAspGluGluPheArg 214
 DB 403 -----TATGACCTCTGGGCACTCC----- 423
 QY 215 AspValArgMetProValAlaAsnProPheProLeuGluArgAlaLeuProCysAspSer 234
 DB 423 ----- 423
 QY 235 AlaArgProValProGlyGluTyrSerArgProThrLeuGluValSerProAsnValCys 254
 DB 423 ----- 423
 QY 255 HisSerAsnIleTyrSerProLeuGluThrIleProGluGluAlaArgSerAspMetHis 274
 DB 423 ----- 423
 QY 275 TyrSerValAlaGluGlyLeuIlePheProAlaAlaProSerAlaArgAsnAlaProTyrPhe 294
 DB 424 -----CTGCGCGCCCTG----- 435
 QY 295 ProCysAspIleValSerIleGluGluArgProSerSerGluAspGluIleAlaLeu 314
 DB 436 -----GAGCAGAACCCCAACA----- 453
 QY 315 HisPheGluProProAsnAlaProLeuAsnArgIleGlyLeuValSerProGlnSerPro 334
 DB 454 -----CCCCCAAGGCGCCCT-----CCACGAGTAACTCC 483
 QY 335 GlnIleSerAspCysGlnProAsnSerProThrGluAlaCysSerSerIleAsnAlaCys 354
 DB 484 AGCGGCTCCAGAGACACCCAGACCCCACTGAACTGAACTGAAAC----- 528
 QY 355 IleLeuGlnAlaSerGlySerProProAlaIleSerProThrAspProLeuAlaCysAsn 374
 DB 529 -----TGCACTCAAGGCCCCCAAGTCAAGCCCTGACCCCAAGGCTGCAAC 579
 QY 375 TrpIleIleTyrIlePheIleValIleuAsnSerLeuAsnAlaIleValProGlyCys 394
 DB 580 TGGAAAAAGTAAAGTAACTGCTTAACTCT----- 612
 QY 395 ProGluGlnAlaGluLeuGlyArgLeuSerProArgAlaTyrThrAlaProProAlaCys 414
 DB 613 -----CAGCCCTCCCAAGAGGAGCGCTGCGGAGAGAAAGTTCTGCTCAACTTGGCCC 669
 QY 415 GlnProProMetGluProGluAsnLeuAspLeuGlnSerProThrIleLeuSerAlaSer 434
 DB 670 CAAGCCAGGCTCCCAAGTGAAGAGAGAGCTCCAGCAGCAGCAGCAGCAGCAGCAGC 729
 QY 435 GlyIleAspSerThrIlePro-----GlnAlaSerArgLeuAsnIleValAsnArgSer 453
 DB 730 AGTAAAGAGAGACCAATTCTCTGCTCCCAAGAGCAGGCTC----- 768

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Title: US-10-755-889-18
Perfect score: 3793
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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+ p2n.model -DEV=xlh
-O=/abse/ABSEWEB.spool/US10755889/runat_01032006_143944_11299/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=p2n.ref -MINMATCH=0.1 -LOOFC=0 -LOOEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCLIN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs806h
-USER=US10755889 @CGN 1.1 4015 @runat_01032006_143944_11299 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hic:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gse1:*
10: gb_gse2:*
11: gb_gse3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	3760	99.1	2985 4	CR858790 Pongo pyg
2	3604.5	95.0	3307 4	AK039228 Mus muscu
3	3598.5	94.9	3289 4	AK036975 Mus muscu
4	3519	92.8	1977 10	AY399831 Homo sapi
5	3351.5	88.4	1980 10	AY399833 Mus muscu
6	2521	66.5	1702 10	AY399832 Pan trogl
7	1493	39.4	920 5	BX431187 BX431187

8	1446	38.1	859 8	CX565176
9	1395.5	36.8	1092 3	BM550970
10	1381.5	35.4	856 5	BO722826
11	1362	35.9	1004 3	BM801045
12	1335	35.2	800 1	AJ454603
13	1331.5	35.1	804 5	BO716058
14	1286	33.9	849 5	BX419860
15	1284	33.9	798 1	AJ441866
16	1274	33.6	830 8	DN285116
17	1262	33.3	867 8	DN286427
18	1248	32.9	690 7	CN401515
19	1215.5	32.0	816 7	CK304021
20	1192	31.4	732 1	AU133895
21	1187	31.3	995 5	BO713052
22	1175	31.0	913 3	BO230532
23	1162	30.6	704 1	AJ398804
24	1157.5	30.5	1425 10	AY415850
25	1154	30.4	772 7	CN401514
26	1151.5	29.0	1443 10	AY415848
27	1132	29.8	840 7	CO573472
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29	1109.5	29.3	822 5	BU404010
30	1100.5	29.0	744 3	BU738471
31	1094	28.8	749 1	AJ454600
32	1091	28.8	617 6	CB132570
33	1090.5	28.8	714 1	AJ396213
34	1080	28.5	942 3	B1599247
35	1075	28.3	666 1	AJ445231
36	1054	27.8	797 1	AJ454599
37	1041	27.4	761 6	CA317787
38	1040	27.4	765 5	BU569071
39	1033	27.1	581 2	BP912750
40	1029.5	27.2	703 1	AJ441724
41	1018	26.8	717 7	CK365134
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ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION Pongo pygmaeus mRNA; CDNA DKFZp46811913 (from clone DKFZp46811913).
ACCESSION
VERSION CR858790.1 GI:55728505
KEYWORDS
SOURCE
ORGANISM

Pongo pygmaeus (orangutan)
Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Pongo.
1 (bases 1 to 2985)
Ottewaelder,B., Obermaier,B., Deutschenbaaur,S., Schappi,A.,
Mewes,H.W., Well,B., Amld,C., Osanger,A., Fobo,G., Han,W., and
Wiemann,S.
The German CDNA Consortium
Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Medigenomix (Martinried/Germany) within the CDNA
sequencing consortium of the German Genome Project.

CONSRMT
TITLE
JOURNAL
COMMENT
This clone (DKFZp46811913) is available at the RZPD Deutsches
Resourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneid=DKFZp46811913
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.

FEATURES

Location/Qualifiers

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/db_xref="taxon:9600"
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DH10B; sites Sfi1A + Sfi1B"
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/gene="DKFZp46811913"
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/protein_id="CAH90995.1"
/db_xref="GI:55728506"
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VARGIKPAASARNAPYPCDKASKEBRSSEBIALHEPBNAPLNKGLVSPSP
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EGPBOALGRLSFRATYAPACOPMEPERLDQSPFKLASGESESTTIPOASTNIV
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ORIGIN

Alignment Scores:
Pred. No.: 8,46e-291 Length: 2985
Score: 3760.00 Matches: 699
Percent Similarity: 99.3% Conservative: 2
Best Local Similarity: 99.0% Mismatches: 5
Query Match: 99.1% Indels: 0
DB: 4 Gaps: 0

US-10-755-889-18 (1-706) x CR658790 (1-2985)

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Db 109 ATGGCTTACCGGCTGACAGCTGTATCCAGTTCACCGCATGCGACGTGATGTTCTTCTC 168
QY 21 AaLLeuAaPnArGLeuAaGSeRaRgAaPILeLeuThRaApVaLlIeVaLlASeRaG 40
Db 169 AACCTTAATGCTCTCCGAGTCGAGACATCTTGACTATGTTGATGTTGAGCGGT 228
QY 41 GluInPheArGaLaHlSlyThVaLLeuMeLaCySeSeRgILeUpHeTySeRILe 60
Db 229 GAGAGATTGAGCGCCATMAAACGCTCTCATGCGCTCGACGTGCGCTGTTCTATAGATC 288
QY 61 PheThRaPnGInLeuLyCyAaLLeuSeRaVlIleAaLLeuAaPProGluIlEaPPro 80
Db 289 TTTCACAGACCGATTGAATGCACTTAGTGTGATCAATCTAGATCCTGAGATCAACCT 348
QY 81 GluInLyPheCySILeLLeuLeuAaPpHeMeTyThSeRaRgLeuAaLLeuAaRgGluI 100
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QY 101 AaLlLeMeLaVaLMeLaAThRaLMeTyLeuGInMeTGuHlSvaLlAaPThR 120
Db 409 AACCTCATGCTGTGATGCGCACAGCTATATGACTGACAGATGAGCATGTTGTGAGACT 468
QY 121 CyAaRgLyPheHlLeLySaLaSeRgLuAaGluMeVaLSeRaLlLeLyPProPArG 140
Db 469 TGCGGAGAGTTTATCAAGGCGACGTGAAGACAGATGATGTTCTTCAACCAAGCCCTCGT 528
QY 141 GluInPheLeuAaPnArGMeLeuMeTProGInPheLlMeLaATyRaRgGlyArG 160
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QY 161 GluVaLlAaGluAaAaPnLeuProLeuAaRgSeRaLlAaPProGlyCySeGluSeRaRgLaPhe 180
Db 589 GAGGTGTGTGAGAAACACCTGCACTGAGAGCGCCCTGGGTGTGAGAGCAGACCTTT 648
QY 181 ALaPSeSeRLeuTySeRgILeUSeRThRProProlASeTySeSeMeTySeRnHs 200
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QY 201 LeuProVaLSeSeSeLeuLeuPheSeRaPnGluInPheArGaPpVaLArGMeTProVaL 220
Db 709 CTCCTGTACAGAGCTCTCTTCTCCATGAGAGGATTTCCGAGATGCTCGGATGCTGTG 768
QY 221 ALaAaPnProPheProLyGluArGLaLeuProCyAaPSeRaLlAaRgProVaLProLy 240
Db 769 GCCAACCCCTTCCCAAGAGAGCGGCTCTCCATGTATGATGCGACGACGCTCTGT 828
QY 241 GluTySeRaRgProThRLeuGluVaLSeRProAaPnVaLcYSHSeSaAaLlEtySeR 260
Db 829 GAGTACAGCGGCGCACTTTGAGAGTGTCTCCCAATGTGTGTACAGCAATATCTATTCA 888
QY 261 ProLySgLuThRlLeProGluGluLlAaRgSeRaPMeThlEtySeRaVaLlAaGluGly 280
Db 889 CCCAAGAAACAGTCCCAAGAGAGCGACGAAGTATATGACTATACAGTGTGCTGAGGAGC 948
QY 281 LeuLyPProAlAlAPSeSeRaLlAaRgAaAaLAProTyRPhPProCyAaPpVaLlAaSeR 300
Db 949 CTCGAAGCTGTGCGCCCTCCACCGCAAAATGGCCCTACTTCCCTTGACAAAGCGCAGC 1008
QY 301 LySgLuGluGluArGProSeSeRgLuAaPpGluIlEaLLeuHlAaPheGluProPProAa 320
Db 1009 AAGAAAGAAAGAGAGACCTCTCAAGATGATGATGCTTCACTTTCAGAGCCCCCAAT 1068
QY 321 ALaProLeuAaPnArGlySgLyLeuVaLSeRProGInSeRProGInLySeRaPcYsGIn 340
Db 1069 GCACCCCTGACACGGAAGGCTGTGTTGATGTCACAGAGCCCCCAGAAATCTGATGCGCAG 1128
QY 341 ProAaPnSeRProThGluLlAaCySeSeRlySaAaLlAaCyLlLeuGInLlAaSeRgLy 360
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QY 381 lLeVaLLeuAaPnSeRLeuAaGInAaAaLlAaPProGlyGlyProGluGluLlAaGluLeu 400
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QY 401 GlYArGLeuSeRProArGAlArThRaLAPProProlAaCyGInPProMeTGuLPro 420
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Db 1369 GAAAGACTTGACTTCAAGTCCCAACCAAGCTCAAGGCCAGGAGGAGACTCCACCATC 1428
QY 441 ProGInAlASeRaRgLeuAaAaLlEaLlAaAaPSeSeMeTThGlySeRProArGSeR 460
Db 1429 CCACAGACAGCGGCTCAATAACATCGTTAAGGTTCATAGACGGGCTCTCCCGCACAC 1488
QY 461 SeSeRgILeUSeRThlASeRProLeuTyMeThlAPProPProLyCyThSeRcYsGlySeR 480
Db 1489 AGCAGGAGAGCACTCACCACTTACATGACACCCCAAGGTGACATCTCGCGGCTCT 1548
QY 481 GInSeRProGInHlAaGluMeTySeLLeuHlSthAlaGlyProThRPhaLaGluGlu 500
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QY 501 MeTGLyGLlThGInSeRgILyTySeRaPSeSeRcYsGILyAaAaGlyLaPhePheCyS 520
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Db 1609 ATGGGAGAGACCCAGTCTGAGTACTCAGATTCCAGCTGTGAGAACGGGCTTCTTCTG 1668

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Qy 541 Hisseraplysprrtylycyasapargyseglnalaserpheargtyrlysglyasn 560

Db 1729 CACAGTACAAACCTTCAAGTGTGACCGCTGCGACGCTCTCCCTCAAGAGGACAC 1788

Qy 561 leualaserishlystrvalhisethrglyglulysprrtyrargyasaenillecyegly 580

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Qy 581 AlaglnpheasnartrproalaaenleuysThrishrargillehseryglulys 600

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Db 2029 CACCTTACAGACTCGAAGAGCCACTCGAGATCCACAGAGAGAAACCTTACATGT 2088

Qy 661 GlulysCyasenleuhsiphearghislysserlglnleuargleuhsleuargGlnlys 680

Db 2089 GAGAAGTGTACCTGCATTTCCGTACAAAGTACAGCTGCAGCTTCACTTCCGCGACAG 2148

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Qy 701 GluleuprrtylAsAlaCys 706

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RESULT 2 AKO39228 3307 bp mRNA linear HTC 03-APR-2004

LOCUS AKO39228 Mus musculus adult male spinal cord cDNA, RIKEN full-length

DEFINITION enriched library, clone:A330001J07 product:B-cell leukemia/lymphoma

ACCESSION AKO39228

VERSION AKO39228.1 GI:26333136

KEYWORDS HTC; CAP trapper;

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 Carninci, P. and Hayashizaki, Y.

AUTHORS High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

PUBMED 10349636

REFERENCE 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

AUTHORS Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to

JOURNAL prepare full-length cDNA libraries for rapid discovery of new genes

PUBMED Genome Res. 10 (10), 1617-1630 (2000)

REFERENCE 3

AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,

Kono, H., Akiyama, J., Nishi, K., Katsunai, T., Teshito, H., Itoh, M.,

Sun, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,

Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,

COMMENT

TITLE

JOURNAL

REFERENCE

AUTHORS

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JOURNAL

REFERENCE

AUTHORS

FEATURES

SOURCE

CDS

Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.

RIKEN Integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

11076861

4 The RIKEN Genome Exploration Research Group Phase II Team and the

PANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection

Nature 409, 685-690 (2001)

5 The PANTOM Consortium and the RIKEN Genome Exploration Research

Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 3307)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,

Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,

Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,

Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,

Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M.,

Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,

Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohnato, N.,

Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,

Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,

Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Kahira, S.,

Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,

Muramatsu, M., and Hayashizaki, Y.

Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of

Biological Sciences, RIKEN, Laboratory for Genome

Physical and Chemical Research (RIKEN), Laboratory for Genome

Exploration Research Group, RIKEN Genomic Sciences Center (GSC),

RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,

Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,

URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,

Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/

Location/Qualifiers

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match=2208)

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polya_site
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ORIGIN

Alignment Scores:

Pred. No.: 3.13e-278 Length: 3307
Score: 3604.50 Matches: 666
Percent Similarity: 96.2% Conservative: 14
Best Local Similarity: 94.2% Mismatches: 26
Query Match: 95.0% Indels: 1
DB: 4 Gaps: 1

US-10-755-889-18 (1-706) x AK039228 (1-3307)

QY 1 MetAlaSerProAlaSerSerCysIleGlnPheThrArgHisAlaSerAspValIleuLeu 20
DB 111 ATGGCCCTCCCGGCTGACACACTGATTCAGTTACCGGACCGCTAGTATGTTCTTCTC 170
QY 21 AsnLeuAsnArgLeuArgSerArgAspIleLeuThrAspValIleValIleSerArg 40
DB 171 AACCTTAATGCTCTCCGAGTCGGACATCTTGAACGACCTTGTCATCGGTGAGCCCGT 230
QY 41 GluGlnPheArgAlaHisIleThrValIleuMetAlaCysSerGlyLeuPheTyrSerIle 60
DB 231 GAGAGATTAGAGCCATTAAGACAGAGCTCATGAGCCCTGACGCGCTGTTCTACAGATAC 290
QY 61 PheThrAspGlnLeuLysCysAsnLeuSerValIleAsnLeuAspProGluIleAsnPro 80
DB 291 TTCACTGACCAAGTTGAAATGCACACTTAAGTAACTAATCTAGATCCTGAAATCAGCCCT 350
QY 81 GluGlyPheCysIleLeuLeuAspPheMetTyrThrSerArgLeuAsnLeuArgGluGly 100
DB 351 GAGGGGTTTTCATCTCCCTGACCTTCATGATACATCTAGGCTCAACCTGAGGGAAGGC 410
QY 101 AsnIleMetAlaValMetAlaThrAlaMetTyrIleuGlnMetGlnHisValIleAspThr 120
DB 411 AATATCATGGGGGTGAGTACACACAGCATGATGACTGAGATGAGCATGTTGTGACACA 470
QY 121 CysArgIysPheIleIleAlaSerGluAlaGluMetValSerAlaIleLysProProArg 140
DB 471 TGCAGGAAGTTCAATCAAGCCAGTGAAGGAGAAATGCCCCCTGACATTAACCTCCCGCT 530
QY 141 GluGlnPheLeuAsnSerArgMetLeuMetProGlnAspIleMetAlaTyrArgGlyArg 160
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QY 161 GluValValIleGluAsnAsnLeuProLeuArgSerAlaProGlyCysGlySerArgAlaPhe 180
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QY 181 AlaProSerLeuTyrSerGlyLeuSerThrProProAlaSerTyrSerMetTyrSerHis 200
DB 651 GCTCTCTCTCTGACATGGGCTCTCAACACACACAGCCCTTATCCCATGTACAGGCAT 710
QY 201 LeuProValSerSerLeuLeuPheSerAspGluGlnPheArgAspVal---ArgMetPro 219
DB 711 CTCCCGCTCAGACACTTCTCTCTCTCTGATGAGAGCTCCGAGATGCCCCCGAATCTCT 770
QY 220 ValAlaAsnProPheProIlysgIuArgAlaLeuProCysAspSerAlaArgProValPro 239
DB 771 GTGGCAACCTTTTCCCAAGAGAGGCTCCCTCCCTGACACAGTGCAGAGCAAGTCCCT 830
QY 240 GluGlyTyrSerArgProThrLeuGlnValSerProAsnValCysHisSerAsnIleTyr 259
DB 259

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QY 280 GlyLeuLysProAlaAlaProSerAlaArgAsnAlaProTyrPheProCysAspIysAla 299
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QY 300 SerIlysgIuGlnIlyArgProSerSerGluAspGluIleAlaLeuHisPheGluProPro 319
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QY 420 ProGluAsnLeuAspIleuGlnSerProThrIlyLysSerAlaSerGlyGluAspSerThr 439
DB 1371 CCGGGAACCTTGAATCTCCAGTCCCGGACCAAGCTCAGTGCAGTGGGAGGACCTTACC 1430
QY 440 IleProGlnAlaSerArgLeuAsnAsnIleValAsnArgSerMetThrGlySerProArg 459
DB 1431 ATCCCCCAAGCCAGCGGTCAATATCTCGGAACAGGCTCCCTGACAGGCTCCCCCGA 1490
QY 460 SerSerSerGluSerHisSerProLeuTyrMetHisProProIlyCysThrSerCysGly 479
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QY 520 CysAsnGluCysAspCysArgPheSerGluGluAlaSerLeuLysArgHisThrLeuGln 539
DB 1671 TCGAAGATGTGATGCTGCGCTTCTCTGAGAGGCTGCTCAAGAGGACAGCGTGCAG 1730
QY 540 ThrHisSerAspIlyProTyrIlyCysAspArgCysGlnAlaSerPheArgTyrIlyGly 559
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Db	113	ATGGCTCCCGCGCTGACAGCTGTATTCACGTTTACC	CGGACAGCTGATGATGTTCTTCTC	172
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Db	173	AACTTATTCCTCCCGAGTCGGGACATCTTTGACGAGCGTTCATCGTGGTGAGCCGT		232
Qy	41	GIuGIuINPheArgAlaHisIleValThrValIleuMetAlaCysSerGlyLeuPheTyrSerIle		60
Db	233	GAGCAGTTTAAAGCCCAATAAGACAGTGTCAATGCGCTCGACGGCCGTCTTCAAGATC		292
Qy	61	PheThrAspGlnLeuLysCysAsnLeuSerValIleAsnLeuAspProGluIleAsnPro		80
Db	293	TTTCACTGACACAGTTGAAATGCACTTATAGTATATCAATCTAGATCTCGAAATCAGCCCT		352
Qy	81	GIuGIuPheCysVilIleuLeuAspPheMetTyrThrSerArgLeuAsnLeuArgGluGly		100
Db	353	GAGGGGTTTTTCATCTCTCTGAGCTTCATGTACACATCTAGGCTCAACCTGAGGGAAGGC		412
Qy	101	AsnIleMetAlaValMetAlaThrAlaMetTyrIleuGlnMetGlnHisValValAspThr		120
Db	413	AATAATCAAGGGGTATGATACCAACAGCCATGTACTGGAAGAGGAGCATGTTGTGCACACA		472
Qy	121	CysArgLysPheIleIleValIleSerGluValIleGluMetValSerAlaIleLysProProArg		140
Db	473	TGCAGAAAGTTTCATCAAGGCCAGTGAACAGAAATGGCCCTCGACATTAACTCCCGCT		532
Qy	141	GIuGIuPheLeuAsnSerArgMetLeuMetProGlnAspIleMetAlaTyrArgGlyArg		160
Db	533	GAAAGGTTCTGTGAACAGCCGGATGCTGATGCCCATGACATCATGGCTTACCGAGTCTGT		592
Qy	161	GIuValIleValGluAsnAsnLeuProLeuArgSerAlaProGlyCysGluSerArgAlaPhe		180
Db	593	GAGGTCGTGGAGAAACAATATGACATCTGAAGAATACTCCGGGTGTGAGAGCAGGCTTTT		652
Qy	181	AlaProSerLeuTyrSerGlyLeuSerThrProProAlaSerTyrSerMetTyrSerHis		200
Db	653	GCTTCTCTCTGTATCATTTGGCTGTCAACACACACAGCCTTTATCCATGTACAGCCAT		712
Qy	201	LeuProValIleSerSerLeuLeuPheSerAspGluGluPheArgAspVal--ArgMetPro		219
Db	713	CTCCCGCTCAGACACTTCTCTCTCTGTATGAGGAGCTCGAGATGCCCCCGAATGCTT		772
Qy	220	ValAlaAsnProPheProPheArgGluArgAlaLeuProCysAspSerAlaArgProValPro		239
Db	773	GTGGGCAACCCCTTTTCCAGAGAGGTGCTCCCTCCCTCGCAGCAGTGCAGCAAGTCCCT		832
Qy	240	GIuGIuTyrSerArgProThrIleuGluValIleSerProAsnValCysHisSerAsnIleTyr		259
Db	833	AATGAGTATGACAGGCCAGCCATGAGAGGTGTCCCCCATTTGTGTACAGACAACTTAC		892
Qy	260	SerProLysGluThrIleProGluGluValIleArgSerAspMetHisTyrSerValAlaGlu		279
Db	893	TGCCCCAAGAGAGCAGTCCACAGAGGAGGCTGGAGTGCATATCACTACAGTGTCCGTGAG		952
Qy	280	GlyLeuLysProAlaAlaProSerAlaArgAsnAlaProTyrPheProCysAspLysVal		299
Db	953	GGCCCCAAGCCTGCTGCTCTCTCTGCGAATGCTTCATCTTCCCTGTCGACAAAGGCC		1012
Qy	300	SerTyrGluGluGluArgProSerSerGlnAspGluValIleAlaLeuHisPheGluProPro		319
Db	1013	ACCAAAAGAAAGAGACATTTCTTCGAGAGATGATGTGCTTCGATTGGAACCCCCC		1072
Qy	320	AsnAlaProLeuAsnArgLysGlyLeuValIleSerProGlnSerProGlnLysSerAspCys		339
Db	1073	AATGCACCTTGAACCGAAGGCTGTGGTTAGTCCCCAGAGATCCCCAGAAATCCGACTGC		1132
Qy	340	GlnProAsnSerProThrGluAlaCysSerSerLysAsnAlaCysVilIleuGlnAlaSer		359
Db	1133	CAGCCCAACTCAACCAAGAGTCTTCGACAGCAGCAAGAACGCTGATCTTCAAGGCTCT		1192
Qy	360	GlySerProProAlaLysSerProThrAspProGlyValAlaCysAsnThrLysLysTyrLys		379
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ACCESSION	genomic survey sequence.					
VERSION	AY399831					
KEYWORDS	AY399831.1 GI:39755820					
SOURCE	GSS.					
ORGANISM	Homo sapiens (human)					
REFERENCE	Homo sapiens					
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.					
TITLE	1 (bases 1 to 1977) Clark,A.G., Glanowski,S., Nelson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shteky,J.J., Adams,M.D. and Cargill,M. Interfering nonneutral evolution from human-chimp-mouse orthologous gene trios Science 302 (5652), 1960-1963 (2003)					
JOURNAL	Science 302 (5652), 1960-1963 (2003)					
PUBMED	14671302					
REFERENCE	2 (bases 1 to 1977) Clark,A.G., Glanowski,S., Nelson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shteky,J.J., Adams,M.D. and Cargill,M. Direct Submission Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA					
AUTHORS	This sequence was made by sequencing genomic exons and ordering them based on alignment.					
COMMENT	Location/Qualifiers					
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Db	1 ATGGCTCGCGCGCGAGCAGCGTGTATCCAGTCACCAGCAATGCATGATGTTCTTCTC 60					
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QY	161	GIUValValGIuBnbnAnLeuProLeuArgSerAlaProGlyGlyGlySerArgAlaPhe	180
Db	481	GAGGTGGTGAAGAACCACTTGCCACTGAGGAGGGCCCTGGGGTGTGAGACAGAGCCTTT	540
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QY	201	LeuProValSerSerLeuLeuPheSerAspGluGluPheArgAspValArgMetProVal	220
Db	601	CTCCCTGTCAAGACGCTCTCTCTCCGATGAGGAGATTTGGGAGTGTCCGGAATGCCGTGTG	660
QY	221	AlaAsnProPheProGlyGlyValArgAlaLeuProCysAspSerAlaArgProValProGly	240
Db	661	GCCAACCCCTTCCCAAGAGGGGCACTCCCATGTGATGTGCAAGGCCAGTCCCTGGT	720
QY	241	GluTyrSerArgProThrLeuGluValSerProAsnValCysHisSerAsnIleTyrSer	260
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QY	401	GlyArgLeuSerProArgAlaTyrThrAlaProProAlaCysGlnProPheGluPro	420
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Db	1261	GAGAACTTGAACCTCCAGTCCCAACCAAGCTGATGTGCAGGGGAGAGATCCACATTC	1320
QY	441	ProGlnAlaSerArgLeuAsnAsnIleValAsnArgSerMetThrGlySerProArgSer	460
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QY	461	SerSerGluSerHisSerProLeuTyrMetHisProPolySyrThrSerCysGlySer	480
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Qy 561 LeuAlaSerHisLysThrValHisThrGlyGluLysPheTyrArgCysAsnIleCysGly 580

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DEFINITION Mus musculus BCL6 gene, VIRUTAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY399833
VERSION AY399833.1 GI:39755822
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE
AUTHORS Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1980)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejaritwal, A.,
Todd, M.A., Tanenbaum, D.M., Civeleo, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adam, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
TITLE 2 (bases 1 to 1980)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejaritwal, A.,
Todd, M.A., Tanenbaum, D.M., Civeleo, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adam, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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US-10-755-889-18 (1-706) x AY399833 (1-1980)

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Db 1 ATGGCTCCCGCGCTGACAGCTGTATCCAGTTTACCGGACGCTAGATGTTCTTCTGC 60

Qy 21 AsnLeuAsnArgLeuArgSerArgAspIleLeuThrAspValIleValAlaSerArg 40

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Qy 41 GlnGlnPheArgAlaHisLysThrValLeuMetAlaCysSerGlyLeuPheTyrSerIle 60

Db 121 GAGCAGTTTAAGCCCATTAAGACAGTGTCAAGTGCCTGACGCGCTGTCTTACAGTATC 180

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Db 181 TTCACGTACACGATTGAATGCACTTGTATGATCAATCTAGATCTGAAATACAGCCCT 240

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Db 241 GAGGGGTTTGGATCCTCCTGGAATTCATGTACATATGAGCTCAACTGAGGAGAGCC 300

Qy 101 AsnIleMetAlaValMetAlaThrAlaMetTyrLeuGlnMetValSerAlaIleLysProArg 120

Db 301 AATATCATGCGGTATGACACAGCCATGATACCTGACAGATGACATGTTGTCAACACA 360

Qy 121 CysArgLysPheIleLysAlaSerGluAlaGluMetValSerAlaIleLysProArg 140

Db 361 TCGAGAGATTATCAAGGCCGATGAGAGCAAAATGCCCCCGCACTTAACTCCCGCT 420

Qy 141 GlnGluPheLeuAsnSerArgMetLeuMetProGlnAspIleMetAlaTyrArgGlyArg 160

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Qy 240 GlyGluTyrSerArgProThrLeuGluValSerProAsnValCysHisSerAsnIleTyr 259

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Db 781 TCGCCCAAGAGAGAGCTCCAGAGAGCTCGAGATGACATACATACATGATGCTGAG 840

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Oy	400	LeuGIuArgLeuSerProArgAlaTrpTrpAlaProProAlaCysGlnProPomErglu	419
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Oy	420	ProGluAsnLeuAspLeuGlnSerProThrLysLeuSerLysAsnArgLysLysAspSerThr	439
Db	1261	CCCCGGAACCTTGAATCTCCAGTCCCGACCAACGTCAGTGCAGATGGAGAGACTTACC	1320
Oy	440	IleProGlnAlaSerArgLeuAsnAlaIleValAsnArgSerMetThrGlySerProArg	459
Db	1321	ATCCCCCAAGCAGCCGGCTCAATATCTCGTGAACAGTCCCTCGAGAGCTCCCCCGA	1380
Oy	460	SerSerSerGIuSerHisSerProLeuTrpMetHisProProLysCysTrpSerCysGly	479
Db	1381	AGCAGCAGTGAAGATCACTCAACCTCAATGACACCCCGCAAGATGCACATCTCGGGCC	1440
Oy	480	SerGlnSerProGlnHisAlaGluMetCysLeuHisIleThrAlaGlyProThrPheAlaGlu	499
Db	1441	TCTCAAGTCCCAACAGCATACAGAAATGGCTCTCAATCTGCTGGAGCCACGTTCCGAG	1500
Oy	500	GluMetGIuGIuThrGlnSerGIuTrpSerAspSerSerCysGIuAsnGIuAlaPhePhe	519
Db	1501	GAGATGGGGGAAACCGACGTCAAGATTTCCGATTCTTAGCTGTGAAATGGACCTTCTTC	1560
Oy	520	CysAsnGIuCysAspCysArgPheSerGIuAlaSerLeuLysArgHisIleThrLeuGln	539
Db	1561	TGCAACGAATGTGACTGCCGTTCTCTGAGAGGCTCTGCTCAAGAGGCACAGCTCGAG	1620
Oy	540	ThrHisSerAspLysProTrpLysCysAspArgCysGlnAlaSerPheAspTrpLysGly	559
Db	1621	ACGCACAGATGACAAACCAATATGATATGCTGCCAGGCTCTCTCCGCTCAACAGGCG	1680
Oy	560	AsnLeuAlaSerHisLysThrValHisIleThrGIuLysProTrpArgCysAsnAlaCys	579
Db	1681	AACCTCCGACACCAACAGACTGTCCACACGGGTGAAACCTTATCGTGAACATTTGT	1740
Oy	580	GlyAlaGlnPheAsnArgProAlaAsnLeuLysTrpHisIleThrArgIleHisSerGIuLys	599
Db	1741	GGAGGCGACTTCAATCGCGCGACGCAACCTGAAAGCCCACTCGAATTCACTCGAGAA	1800
Oy	600	LysProTrpLysCysGIuThrCysGIuAlaArgPheValGlnValAlaHisLeuArgAla	619
Db	1801	AAGCCCTCAATATGAAACCTGTGGGGCCAGGTTTGTTCAGTGGGCCCACTCCGTC	1860
Oy	620	HisValLeuIleHisIleThrGIuLysProTrpCysGIuIleCysGIuThrArgPhe	639
Db	1861	CACGTGCTCATCACTGAAAGAGAGCGATCCCTGTGAATGTGTGGCACTCGCTTC	1920
Oy	640	ArgHisLeuGlnThrLeuLysSerHisLeuArgIleHisIleThrGIuLysProTrpHis	659
Db	1921	CGGCACTTCAAGACTGAAAGGCATGTGGCATTCACACAGAGAGAAACCTTACAT	1980

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LOCUS	AY399832				
DEFINITION	Pan troglodytes BCL6 gene, VIRUTAL TRANSCRIPT, partial sequence,				
ACCESSION	AY399832				
VERSION	AY399832.1				
KEYWORDS	GI:39755821				
SOURCE	GSS.				
ORGANISM	*Pan troglodytes (chimpanzee)				
	Pan troglodytes				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;				
	Hominidae; Pan.				
REFERENCE	1 (bases 1 to 1702)				
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,				
	Todd,M.A., Tenenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,				
	Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,				
	Adams,M.D. and Cargill,M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous				
	gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBLISHED	14671302				
REFERENCE	2 (bases 1 to 1702)				
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,				
	Todd,M.A., Tenenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,				
	Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,				
	Adams,M.D. and Cargill,M.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,				
	Rockville, MD 20850, USA				
COMMENT	This sequence was made by sequencing genomic exons and ordering				
	them based on alignment.				
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	/db_xref="taxon:9598"				
	<1...>1702				
	/gene="BCL6"				
	/locus_tag="HCM0355"				
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	Alignment Scores:				
	Pred. No.: 1,366-191 Length: 1702				
	Score: 2521.00 Matches: 488				
	Percent Similarity: 86.4% Conservative: 2				
	Best Local Similarity: 86.1% Mismatches: 77				
	Query Match: 66.5% Indels: 0				
	DB: 10 Gaps: 0				
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Db	1 TGGCCNNCTGAGACGTGTATTCAGATTCAACC GCCCATCGCAGTGAITTTCTNNCCNNTT 60				
OY	23 AenaTgLeuArSerArSpIleleuthrAspValIleIeVaIaIsarAgJugln 42				
Db	61 ATTCGTCTCCGAGAANNMAGACATCTNGNNTGATGTGTGCATTTGTSTGAGCCVTGAGCAG 120				
OY	43 PheatrgAlahLyluethrValIeuMetAlAcYsSeGlyIleuPheryTerIlePeThr 62				
Db	121 TTTAGAGGCCCATMAAACGCTCTCAATGCGCTCCAGAGCGCTGTCTTAAGCACATTTACA 180				
OY	63 AspgIlnLeuLYeCYsaInLeuSerValIlleAnIleuAspProGlIuIleAsnProGlIy 82				
Db	181 GACCACTTAAATATGCACCTTGATGTGATCAATCTAGATCTGAGATCAACCTGAGGGA 240				
OY	83 PheCYslleLeuIleuAspRhemetyTrhrTSerArgLeuAsnIleuArGtJugIyaenlle 102				
Db	241 TTCGTGATCTCTCGGACTTTATGTACACATCTCGGCTCAATTTGGCGGAGGCAATC 300				
OY	103 MetAlaValMetAlAThrAlametyTrLeuGImeGluHlsIvalValasrThrCYsaTy 122				

Db 301 ATGGCTGTATGGCCAGCGCTATGTACTGACAGATGAGCATGTTGTGACACTTGCCTGG 360
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 Db 361 AAGTTATTAAAGCCAGNNNAG 420
 Qy 143 PheLeuA1aSerArgMetLeuMetProGluA1aP11eMeA1aTyrArgG1yArgGluA1 162
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 Qy 183 SerLeuTyrSerG1yLeuSerThrProProA1aSerTyrSerMetTyrSerHisLeuPro 202
 Db 541 AGCCTGTACAGTGGCTGTCCANNACGCCAGCCNNNNATTCACATGACAGCCACCTCCCT 600
 Qy 203 ValSerSerLeuLeuPheSerA1aP11eMeA1aPheArgA1aPheArgA1aPheA1aA1a 222
 Db 601 GTGAGAGAGCTCTCTTCTCCGATGAGAGAGTTCCGGAGTCCGGATGCCCTGTGCGCAAC 660
 Qy 223 ProPheProG1yG1uArgA1aLeuProCyA1aPheSerA1aArgProValProG1yG1uTyr 242
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 Qy 243 SerArgProThrLeuGlu1aSerProA1aPheHisSerA1a1eTyrSerProG1yS 262
 Db 721 AGCCGCGCAGCTTGTGAGGTGTCCCAATGTGTGCACAGCAATATCAATTAACCAAG 780
 Qy 263 GluThr11eProG1uGluA1aArgSerA1aPheMetHisTyrSerA1a1aGluG1yLeuA1y 282
 Db 781 GAAGAAGTCCCAAGAAGGCAACAAGATATCACTACAGTGTGCTGAGGCGCTCAAG 840
 Qy 283 ProA1a1aProSerA1aArgA1aPheTyrPheProCyA1aPheA1aSerG1yG1u 302
 Db 841 CTGTGCTGCCCCCTCAGCCCAAAATGCCCCCTACTTCTGTGTGACAAAGCCACAAAGAA 900
 Qy 303 GluGluA1aProSerSerG1uA1aPheG1u11eA1aPheG1uP1aProA1aA1aPro 322
 Db 901 GAAGAAGAGACCTCTCTGGAAGATGATGATGCTCCATTTTCAAGCCCCCAATGACACC 960
 Qy 323 LeuA1aArgG1yLeuValSerProG1uSerProG1u1ySerA1aPheArgA1aPheA1a 342
 Db 961 CTGAACCGGAAGGCTGTGTTAGTCCACAAGCCCCCAAGAAATCTAGCTCCAGCCCAAC 1020
 Qy 343 SerProThrG1uA1aCySerSerTyrA1aPheA1aCy11eLeuG1uA1aSerG1ySerPro 362
 Db 1021 TCGCCCAAGAGTCTGTCAAGATGATGATGCTCCATCTCCAGGCTTGTGCTCCCT 1080
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 Qy 383 LeuA1aSerSerLeuA1aPheA1aPheProG1yG1yProG1uG1uA1aG1uLeuG1yArg 402
 Db 1141 CTCAACAGCTCTCAACCAAGATGCAACCAAGAGGCGCTGAGAGCTGTGAGCGCGC 1200
 Qy 403 LeuSerProArgA1aTyrThrA1aProProA1aCyG1uA1aPheProMetG1uProG1uA1a 422
 Db 1201 CTTTCCCAAGAGCTTACAGGCGCCCACTGTGCGCAAGCAACCATGAGAGCTGTGAAC 1260
 Qy 423 LeuA1aPheG1uSerProThrTyrLeuSerA1aSerG1yGluA1aPheSerThr11eProG1u 442
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 Qy 443 Al1SerArgLeuA1aPheA1aPheA1aPheA1aPheA1aPheA1aPheA1aPheA1aPhe 462
 Db 1321 GCCAGCGCGCTCAATTAATCTGTTAATCAAGTCAATGAGGCTCTCCCGCAGAGAGAGC 1380
 Qy 463 GluSerHisSerProLeuTyrMetHisProProG1yCyA1aPheSerCyG1ySerG1uSer 482
 Db 1381 GAGAGCCACATCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440

Qy 483 ProG1uH1eA1aGluMetCyLeuH1ePheA1aG1yProThrPheA1aG1uG1uMetG1y 502
 Db 1441 CCACAGACGACGAGATGTGCTCCACACCGCTGACCCCAAGTCTCCAGAGAGATGGGA 1500
 Qy 503 GluThrG1uSerG1uTyrSerA1aPheSerCyG1uA1aPheA1aPheA1aPheA1aPhe 522
 Db 1501 GAGACCCAGTCTGATCTACATGATCTAGCTGTGNNNNNNNNNNNNNNNNNNNNNNNN 1560
 Qy 523 CyA1aPheCyA1aPheSerG1uGluA1aSerLeuA1aPheA1aPheA1aPheA1aPhe 542
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 Qy 543 A1aPheProTyrLeuCyA1aPheArgCyG1uA1aPheA1aPheA1aPheA1aPheA1a 562
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 Qy 563 SerHisTyrThrValHisThr 569
 Db 1681 AGCCACAGAGCCGTCCATACC 1701
 Db
 RESULT 7
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 LOCUS BX431187 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
 DEFINITION CS0DF021YF19 5-PRIME, mRNA sequence.
 ACCESSION BX431187
 VERSION BX431187
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo
 1 (bases 1 to 920)
 LI'W.B., Gruber,C., Jesse,J. and Polayes,D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 JOURNAL
 COMMENT
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
 was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 This sequence belongs to sequence cluster 2184.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?c=CS0BAP016ZC05_AF01476_1&c=2184.r

FEATURES
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 /organism="Homo sapiens"
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 /tissue_type="FETAL BRAIN"
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 /note="Organ: Brain; Vector: pCMVSPORT 6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-strand cDNA was digested with Not I and
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6
 vector. Library was not normalized."

ORIGIN
 Alignment Scores:
 Pred. No.: 2,19e-109 Length: 920
 Score: 1493.00 Matches: 287
 Percent Similarity: 94.1% Conservative: 2
 Best Local Similarity: 93.5% Mismatches: 17
 Query Match: 39.4% Indels: 2

DB: 5 Gaps: 0

US-10-755-889-18 (1-706) x BX431187 (1-920)

QY 211 GluGluPheArgAspValArgMetProValAlaAsnProPheProGlyArgAlaLeu 230

DB 2 GAGGAGTTTCGGAGATGCCGATGCTTGAGNCAACCCCTTCCAG-GAGCGGCACTC 60

QY 231 ProCysAspSerAlaArgProValProGlyValuTySerArgProThrLeuGluValSer 250

DB 61 CCATGATGATGTCCAGCGCCAGTCCCTGGAGAGACCGCGCCGACTTGGAGGTCTCC 120

QY 251 ProAsnValCysHisSerAsnIleTySerProGlySerGluThrIleProGluGluAlaArg 270

DB 121 CCCAATGTGTGCCACGCAATATCTATTCACCCAGAGAAACAATCCAGAGAGGCGACGA 180

QY 271 SerAspMetHisGlyTySerValAlaGluGlyLeuValProAlaAlaProSerAlaArgAsn 290

DB 181 AGGATATGACATACAGTGTGGCTGAGGAGCTTCAAACTGCTGCCCTTACCCCGAAAT 240

QY 291 AlaProTyArgPheProCysAspValAlaSerTySerGluGluArgProSerSerGluAsp 310

DB 241 GCCCCCTACTTCCCTTGTGACAGGCCAGCAAGAAAGAGAGACCTCTCGAGAGAT 300

QY 311 GluIleAlaLeuHisPheGluProProAsnAlaProLeuAsnArgTyGlyLeuValSer 330

DB 301 GAGATGCCCTGCAATTCGAGCCCCCAATGCAACCTCGAAACCGAGGCTGTGGTAGT 360

QY 331 ProGluSerProGluTySerAspCysGluProAsnSerProThrGluAlaCysSerSer 350

DB 361 CCACAGAGCCCCCGAAATCTGACTGCGACGCCCAACTGCGCCACAGAGTCTCGAGCAT 420

QY 351 LysAsnAlaCysIleLeuGlnAlaSerGlySerProProAlaTySerProThrAspPro 370

DB 421 AAGATGCTGTCATCTCCAGGCTTGTGGCTCCCTCCAGCAGAGACCCACATGACCCC 480

QY 371 LysAlaCysAsnTrpTySerTyLysPheIleValLeuAsnSerLeuAsnGlnAsnAla 390

DB 481 AAGCCTGCACTGGAAGAAATACAGTTCATGCTGCTCAACAGCTCAATCAGAAATGCC 540

QY 391 LysProGlyGlyProGluGlnAlaGluLeuGlyArgLeuSerProArgAlaTyThrAla 410

DB 541 AAACCAAGAGGGCTGAGCAGGCTGAGCTGAGCGCTTCTCCACAGAGCTTACACGAGNC 600

QY 411 ProProAlaCysGlnProPheMetGluProGluAsnLeuAsnLeuGlnSerProThrIys 430

DB 601 NCACCTGCTGCGACCCACCATGAGCTGAGAACTTGAACCTTCACTCCCAACCAAG 660

QY 431 LeuSerAlaSer-GlyLeuAspSerThrIleProGlnAlaSerArgLeuAsnAsnIleVal 450

DB 661 CTGAGTGCAGCGGAGGAGACTCCACATCCCAAGAGCCGCGCTCATTAACATCGT 720

QY 450 LAsnArgSerMetThrGlySerProArgSerSerSerGluSerIleHisSerProLeuTyMe 470

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QY 470 HisProProLysCysThrSerCysGlySerGlnSerProGlnHisAlaGluMetCysLe 490

DB 781 GCACCCCGCCAGAGTGCACGTTCTGCGGTTCTCATGTCACAGCATGCAAGAGATGTGCT 840

QY 490 uHisThrAlaGlyProThrPheAlaGluGluMetGlyGluThrGlnSerGluTySerAs 510

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QY 510 pSerSerCysGluAsnGly 516

DB 901 TTCTAGCTGGAGAGACGGG 919

RESULT 8

CX565176 859 bp mRNA linear EST 12-JAN-2005

LOCUS CX565176

DEFINITION UT-M-HA0-cuj-f-01-0-UT.r1 NIH_BMAP_HA0 Mus musculus cDNA clone IMAGE:6735458 5', mRNA sequence.

ACCESSION CX565176

VERSION CX565176.1 GI:57592205

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 859)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE NIH-MGC National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabbs-rc@mail.nih.gov

Tissue Procurement: Dr. James Lin University of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at <http://genome.uiowa.edu/distribution/mouse1.html>

This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: pYX-5.

Location/Qualifiers

1..859

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6"

/db_xref="taxon:10090"

/clone="IMAGE:6735458"

/tissue_type="whole eye"

/dev_stage="embryo 12.5,13.5,14.5 dpc"

/lab_host="DH10B (T1 phage resistant)"

/clone_1ib="NIH_BMAP_HA0"

/note="Organ: Eye; Vector: pYX-Asc; Site 1: Ecor I; Site 2: Not I; The library was constructed according to Bontade, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with Ecor I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is TTAATGAGT. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemlin Chin, Ph.D., program coordinator."

ORIGIN

Alignment Scores:

Pred. No.: 1,18e-105 Length: 859

Score: 1446.00 Matches: 266

Percent Similarity: 95.4% Conservative: 3

Best Local Similarity: 94.3% Mismatches: 13

Query Match: 38.1% Indels: 0

DB: 8 Gaps: 0

US-10-755-889-18 (1-706) x CX565176 (1-859)

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DB 14 GTGCTGAGGGGCCCAAGCTGCTGCTCTTCTGCTCTGAGATGCTCATCTCCCTGT 73

QY 297 AspValAlaSerTySerGluGluGluArgProSerSerGluAspGluIleAlaLeuHisPhe 316

DB 74 GACAAAGCCAGCAAG 133

QY 317 GluProProAsnAlaProLeuAsnArgTyGlyLeuValSerProGlnSerProGlnIys 336

DB 134 GAGCCCCCAATGACACCTTGAACCGGAGAGGTGTGTTGTGCTCCAGAGTCCCAAGAA 193

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Qy 337 SerAspCysGlnProAlaSerProThrGluAlaCysSerSerIysAsnAlaCysIleLeu 356
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Qy 357 GlnAlaSerGlySerProProAlaIysSerProThrAspProIysAlaCysAsnTrpLys 376
Db 254 CAGGCGCTGCGCTCTCCGCGCAGCAAGAGCCCACTGACCCGCAAGCCTGCACTGGAAG 313
Qy 377 LysTyrLysPheIleValLeuAsnSerLeuAsnGlnAsnAlaIysProGlyGlyProGlu 396
Db 314 AACTATAAGATTCAATCGTTCTCAACAGCTTCACAAATCAAGATGCCAAACCCGAGGCTCTGAG 373
Qy 397 GlnAlaGluLeuGlyLysGlnSerProArgAlaTyrThrAlaProProAlaCysGlnPro 416
Db 374 CAGGCAAGCTGGGTGCGCTCTCCCTCGAGCTTACCTGACCGCCGCTTCCAGCGG 433
Qy 417 ProMetGluProGluLeuAsnLeuAsnLeuAsnSerProThrLysLeuSerAlaSerGlyGlu 436
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Qy 437 AspSerThrIleProGlnAlaSerArgLeuAsnAsnIleValAsnArgSerMetThrGly 456
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Qy 457 SerProArgSerSerSerGlnSerIysSerProLeuTyrMetHisProPolysCysThr 476
Db 554 TCCCGCCGAGCGAGCTGAGTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 613
Qy 477 SerCysGlySerGlnSerProGlnIleAlaGluMetCysLeuHisThrAlaGlyProThr 496
Db 614 TCCGCGGCTCTGAGTCCCGCAGCAGATACAGAGATGCTCCATATCTGCTGGGCCAGC 673
Qy 497 PheAlaGluLeuMetGlyGlyThrGlnSerGlyTyrSerAspSerSerCysGluAsnGly 516
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Qy 517 AlaPhePheCysAsnGluCysAspCysArgPheSerGlnGluAlaSerLeuLysArgHis 536
Db 734 ACCTTCTTTCGCAACGATGTAGTCTGCTTCTGAGAGGCTCTGCTCAAGAGGAC 793
Qy 537 ThrLeuGlnThrHisSerAspLysProTyrLysCysAspArgCysGlnAlaSerPheArg 556
Db 794 ACGGTGAGAGCAGCACTGACTAACAACATATGATCTCTGCGCAGGCTCTCTTCGCG 853
Qy 557 TyrLys 558
Db 854 TACAAG 859

RESULT 9
LOCUS BMS50970 1092 bp mRNA linear EST 20-FEB-2002
DEFINITION AGENCOURT_6544992 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5738450
5', mRNA sequence.
ACCESSION BMS50970
VERSION BMS50970.1 GI:18787602
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 1092)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rgs@bms-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:

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FEATURES
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    High quality sequence stop: 635.
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            /clone="IMAGE:5738450"
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            /lab_host="DH10B (phage-resistant)"
            /note="Organ: small intestine; Vector: pCMV-SPORT6;
            site 1: NotI; site 2: SalI; Cloned unidirectionally;
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            enriched for full-length clones and constructed by Life
            Technologies. Note: this is a NIH_MGC Library."

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ORIGIN

Alignment Scores:

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pred. No.: 1,976-101 Length: 1092
Score: 1395.50 Matches: 293
Percent Similarity: 89.74 Conservative: 12
Best Local Similarity: 86.24 Mismatches: 24
Query Match: 36.84 Indels: 11
DB: 3 Gaps: 4

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US-10-755-889-18 (1-706) x BMS50970 (1-1092)

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Db 75 ATGGCTCGCGCGGTGACAGCTGATCCAGTTCACCCGCGCAGTCCAGTATGTTCTTCTC 134
Qy 21 AsnLeuAsnArgLeuAsnArgSerArgAspIleLeuThrAspValIleValIysArg 40
Db 135 AACCTTAATCGTCTCCGAGTCAAGATCTGACATGATGTTGATGTTGAGCGCT 194
Qy 41 GlnGlnPheArgAlaHisLysThrValLeuMetAlaCysSerGlyLeuPheTyrSerIle 60
Db 195 GACAGCTTTAGAGCCCATTAACCGTCTCTCAAGCTGAGCTGAGGCTGTTCTATAGCATC 254
Qy 61 PheThrAspGlnLeuLysCysAsnLeuSerValIleAsnLeuAspProGluIleAsnPro 80
Db 255 TTTACAGACAGATTGAATAGCAACCTTAGTGTGATCACTGATCTGATCTGATCAACCT 314
Qy 81 GlnGlyPheCysGlyIleLeuLeuAspPheMetTyrThrSerArgLeuAsnLeuArgGlnGly 100
Db 315 GAGGATTCGTGATCTCTCTGAGCTTCATGATCAACATCTCGGCTCAATTGCGAGAGGC 374
Qy 101 AsnIleMetAlaValMetAlaThrAlaMetTyrLeuGlnMetGluHisValIleAspThr 120
Db 375 AACATATGCTGTGTATGATGCGCAGCTATGATCTGACATGAGATGTTGTGACACT 434
Qy 121 CysArgLysPheIleValAlaSerGlnAlaGluMetValSerAlaIleLysProArg 140
Db 435 TCCGGAAGATTATTAAGCCAGTGAAGCAGATGTTTCTGCCATCAAGCTCTCTCGT 494
Qy 141 GlnGlnPheLeuAsnSerArgMetLeuMetProGlnAspIleMetAlaTyrArgGlyArg 160
Db 495 GAAGAGTTCCTCAACGCGCGAGTGTGATGCCCAAGATCAATGCGATGCGGTCGT 554
Qy 161 GluValValGluAsnAsnLeuProLeuArgSerAlaProGlyCysGlnSerArgAlaPhe 180
Db 555 GAGGTGTGAGAACAACTTCCACTGAGAGAGCGCCCTGGGTGTAGAGCAGAGCTTT 614
Qy 181 AlaProSerLeuTyrSerGlyLeuSerThrProProAlaSerTyrSerMetTyrSerHis 200
Db 615 GCCCGCAGCTGTACAGTGGCTGTGCACACCGCCGCTTATTCATGTACACCGAC 674
Qy 201 LeuProValSerSerLeuLeuPheSerAspGluGlnPheArgAspValIysMetProVal 220
Db 675 CTCCTGTGACGAGCTCTCTCTTCTCGATGAGAGATTTGCGGATGTCGAGTCTGTG 734

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QY 221 AlaAsnProPheProlysgluArgAlaLeuProCysAspSerAlaArgProValProGly 240
 DB 735 GCCAACCCTTCCCGGAGCGGCACTCCCAAGTATGATGTCAGGCGAGCTCTGT 794
 QY 241 GltTyrSerArgProThr-LeuGluValSer-ProAsnValCysHisSerAsnIleTyrS 260
 DB 795 GAGTACGCGCGGCACTTTTGAGGTCTCCCGCAAGGGGTGCCACAGCAATATCTATT 854
 QY 260 eProlYsgluThrIleProgluGluAlaArgSerAspMetHisTyrSerValAla---G 279
 DB 855 CCCCCAAGAAACATTCCTCCAAAGAGCCACCAATGATATGCTTCAACGGGGGCTGA 914
 QY 279 luGluLeuYsProla--AlaProSerAlaArgAsnAla-ProTyrPheProCysAspL 298
 DB 915 GGGGCTTCAACCTGTGTGCTTCAACCGAAAGCCCTCTACTTCCCTTGAGCA 974
 QY 298 YsAla-SerYsgluGluArg-----ProSerSerGluAspGluIleAlaLeuHis 315
 DB 975 AGGCCCCCAAGAAAAAAGAAAGACCTTCTCCGAAAAATMAAATTTGCCCTGGAT 1034
 QY 316 PheGluProProAsn---AlaProLeuAsn---ArgYsgluLeuVal 329
 DB 1035 TTTCAAGCCCCCAATGGGCCCCCTTAAACCGAAAGGCTTGTG 1082
 RESULT 10
 BQ722826 856 bp mRNA linear EST 16-JUL-2002
 LOCUS BQ722826
 DEFINITION AGENCOURT 8241329 Lupski symptomatic trunk Homo sapiens cDNA clone
 IMAGE:6187194 5', mRNA sequence.
 VERSION BQ722826.1 GI:21861723
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 856)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: Dr. James R. Lupski
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LMU)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LMU at:
 http://image.llnl.gov
 Plate: LAM13580 row: m column: 19
 High quality sequence stop: 637.
 Location/Qualifiers
 1..856
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6187194"
 /sex="male"
 /tissue_type="sympathetic trunk"
 /dev_stage="adult, 16 yr"
 /lab_host="DH10B"
 /clone_lib="Lupski symptomatic trunk"
 /note="Vector: pCMV-SPORT6 (Life Technologies); Site 1:
 NotI; Site 2: SalI; cDNA made by oligo-dT priming.
 directionally cloned using the following adaptors:
 5'-TCGACCAAGCGCTCCG-3' and
 5'-GACTAGTCTAGATCGGACGCGCCCT(15)-3'. Size selected >
 1 kb for average insert length 1.9 kb. This is a primary
 library non-amplified. Library constructed by Life
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
 College of Medicine); available through Life
 Technologies."

ORIGIN
 Alignment Scores:
 Pred. No.: 1,79e-100 Length: 856
 Score: 1381.50 Matches: 274
 Percent Similarity: 97.9% Conservative: 3
 Best Local Similarity: 96.8% Mismatches: 1
 Query Match: 36.4% Indels: 5
 DB: 5 Gaps: 1
 US-10-755-889-18 (1-706) x BQ722826 (1-856)
 QY 60 IlePheThrAspGluLeuYsCysAsnLeuSerValIleAsnLeuAspProGluIleAsn 79
 DB 3 ATCTTACAGACCAAGTTGAATGCACTTAAGTGTATGATCATGATCTGATGATCAAC 62
 QY 80 ProGluGluPheCysIleLeuLeuAspPheMetTyrThrSerArgLeuAsnLeuArgGlu 99
 DB 63 CTGAGGAGATTGTGATCTCTCTGACTTCATGATACATCTCGGCTCAATTGCGGAG 122
 QY 100 GlyAsnIleMetAlaValMetAlaThrAlaMetTyrLeuGluMetGluHisValAsp 119
 DB 123 GGCACATCATGCTGTGATGGCCAGCGCTATGACTGTGAGATGAGCATGTTGTGAC 182
 QY 120 ThrCysArgLysPheIleYsAlaSerGluAlaGluMetValSerAlaIleLysProPro 139
 DB 183 ACTTCCGAGAGATTATTAGGCCAGTGAAGCAGATGTTCTGCCATCAAGCTTCT 242
 QY 140 ArgGluGluPheLeuAsnSerArgMetLeuMetProGluAspIleMetAlaTyrArgGly 159
 DB 243 CTGGAAGAGTTCTCAACAGCCGAGATCTGATGCCCAAGACATCATGCGGGGT 302
 QY 160 ArgGluValValGluAsnAsnLeuProLeuArgSerAlaProGlyCysGluSerArgAla 179
 DB 303 CGTGAAGTGTGTGAAGAACCTGCACTGAGAGCCCTGGGTGTGAGAGCAGAGCC 362
 QY 180 PheAlaProSerLeuTyrSerGlyLeuSerThrProProlaSerTyrSerMetTyrSer 199
 DB 363 TTTGCCCCCAGCTGTGACATGGCTGTCCACCGCCAGCTTTTTCATATACAGC 422
 QY 200 HisLeuProValSerSerLeuLeuPheSerAspGluLupPheArgAspValArgMetPro 219
 DB 423 CACTTCTCTGACAGACCTCTCTTCTCCGATGAGAGTTTGGGATGTCGATGCT 482
 QY 220 ValAlaAsnProPheProlysgluArgAlaLeuProCysAspSerAlaArgProValPro 239
 DB 483 GTGGCAACCCCTTCCCAAGAGCGGCACTCCCATGTGATGTCAGGCCAGTCCCT 542
 QY 240 GlyGluTyrSerArgProThrLeuGluValSerProAsnValCysHisSerAsnIleTyrS 259
 DB 543 GGTAGTACAGCCCGCGCACTTGGAGGTGTCCCAATGTGTCCACAGCAATATCTAT 602
 QY 260 SerProlysgluThrIleProgluGluAlaArgSerAspMetHisTyr-SerValAlaG 279
 DB 603 TCACCAAGAAACATTCCTCCAAAGAGCCACGAATGATATGACTCCCAATGTGGCTGA 662
 QY 279 uGluLeuYsProlaAlaProSerAlaArgAsnAlaProTyrPheProCysAspLysAl 299
 DB 663 GGGCTCAACCTGCTCTCCCTCAGCCCAAGAGCCCTTCTCTTGTGACAGGC 722
 QY 299 AserYsgluGluGluArgProSerSerGluAspGluIleAlaLeuHisPheGluProP 319
 DB 723 CAGCAAGAAAGAAAGAGACCTTCTCGGAAGATGATGCTTGCATTTGAGCCCCC 782
 QY 319 AsnAlaProLeu--AsnArgLysGlyLeu-ValSerPro---GlnSerProGluLysSe 337
 DB 783 CAATGACCTCTGAAACCGAAAGGTCTGGTTAGTCCACAGAACCCCGAGAAATC 842
 QY 337 T 337
 DB 843 T 843
 RESULT 11

BM801045
 LOCUS BM801045 1004 bp mRNA linear EST 05-MAR-2002
 DEFINITION AGENCOURT_6422527 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5586337
 5' mRNA sequence.
 ACCESSION BM801045
 VERSION BM801045.1 GI:19117868
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 1 (bases 1 to 1004)
 NIH-MGC <http://mgs.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LHAM1354 row: b column: 02
 High quality sequence stop: 608.
 Location/Qualifiers

FEATURES

source

1. 1004
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5586337"
 /tissue_type="embryonal carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: testis; Vector: PCMV-SPORE6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 2.5 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 8.5e-99 Length: 1004
 Score: 1362.00 Matches: 279
 Percent Similarity: 87.9% Conservative: 4
 Best Local Similarity: 86.6% Mismatches: 10
 Query Match: 35.9% Indels: 29
 DB: 3 Gaps: 3

US-10-755-889-18 (1-706) x BM801045 (1-1004)

QY 160 ArgGluValAlaGluAAsnLeuProLeuArgSerAlaProGlyCysGluSerArgAla 179
 Db 1 CGTGAAGTGTGTGAGAACAACTGCACTAGAGAGCCCTGTGTGTGAGACAGAGCC 60
 QY 180 PheAlaProSerLeuTyYSerGlyLeuSerThrProProAlaSerTyYSerMetTyYSer 199
 Db 61 TTGTGCCCCGACCTGTGACGTGGCTGTCCACACCGGACCTCTTATTCATGTACAGC 120
 QY 200 HisLeuProValSerSerLeuLeuPheSerAspGluGlnPheArgAspValArgMetPro 219
 Db 121 CACTCTCCCTGTGACACCTCTCTCTTCCGATGAGAGATTTCGGATGTCCGATGCCCT 180
 QY 220 ValAlaAsnProPheProTyYSGluArgAlaLeuProCysAspSerAlaArgProValPro 239
 Db 181 GTGGCCAAACCTTCCCAAGAGCGGCACTCCCATGTATAGTGCACAGCCAGTCCCT 240
 QY 240 GlyGluTyYSerArgProThrLeuGlnValSerProAsnValCysHisSerAsnIleTyY 259
 Db 241 GGTGATGACAGCGCGGCACTTGTGAGGTGTCCCAATGTGTGACACAGCAATATCTAT 300

QY 260 SerProTyYGluThrIleProGluGluAlaArgSerAspMetHisTyYSerValAlaGlu 279
 Db 301 TCACCCAAAGAAACATCCACAGAGGACAGCAATGATATATCACTACAGTGTGCTGAG 360
 QY 280 GlyLeuTyYProAlaIleProSerAlaArgAsnAlaProTyYProPheProCysAspTyYAla 299
 Db 361 GGCCTCAACCTGTGCGCCCTCCACAGCCGAAATGCTTACTCTCTTGTGACAGAGCC 420
 QY 300 SerTyYSGluGluGluArgProSerSerGluAspGluIleAlaLeuHisPheGluProPro 319
 Db 421 ACACAAAGAAAGAGAGACCTCTCTCGAAGATGATGCTTCCCTGATTTGAGGCCCCC 480
 QY 320 AsnAlaProLeuAsnArgTyYSGlyLeuValSerProGlnSerProGlnTyYSerAspCys 339
 Db 481 AATGACACCTTAACCGAGAGGCTCGGTATGTCCACAGAGCCCCAGAAATCTGATGCG 540
 QY 340 GlnProAsnSerProThrGluAlaCysSerSerTyYAsnAlaCysIleLeuGlnAlaSer 359
 Db 541 CAGCCCACTCCGCCACAGAGCTGTGACAGCATGAAGATGCTTGCATCTCCAGGCTCT 600
 QY 360 GlySerProProAlaIleTyYSerProThrAspProTyYAlaCysAsnTyYLeuTyYTyY 379
 Db 601 GGCTCCCTCCAGCCAGAGGCCCACTGACCCCAAGCCTGCACTGGAGAAATACAG 660
 QY 380 PheIleValLeuAsnSerLeuAsnGlnAsnAlaTyYPro-GlyGlyProGluGlnAla-G 399
 Db 661 TTCATGTGTCTCAACAGCTCATGAGATGCAACACAGAGGGGCGCTGACAGGCGCTG 720
 QY 399 IuLeuGlyArgLeuSerProArgAlaTyYThr-AlaProProAla-CysGlnProProMet 418
 Db 721 ACTGGGCGCGCTTTTCCACAGGCTTACACGCGGCCCACTGCGCTGACAGCCCAT 780
 QY 418 rGluProGlu-AAsnLeu-AspLeuGlnSerProThr-LysLeuSer-----AlaSerG1 435
 Db 781 GGAAGCCGAAACCTTGTGACCTCCAGTCCCAACCTTGGAAGTCCCGCGGCGG 840
 QY 435 yGluAspSerThrIleProGlnAlaSerArgLeuAsnIleValAsnArgSerMetW 455
 Db 841 AGGACTTCCCATTTCC----- 859
 QY 455 rGlySerProArgSerSerSerGluSerHisSerProLeuTyYMetHisPro 472
 Db 860 -----CCCAAGCCAGCCCGGCTGACATGAA-----CATGCC 892

RESULT 12

AJ454603/C AJ454603 900 bp mRNA linear EST 22-APR-2002
 LOCUS AJ454603 riken1 gallus gallus cDNA clone 3d2082, mRNA sequence.
 DEFINITION AJ454603
 ACCESSION AJ454603
 VERSION AJ454603.1 GI:20264699

KEYWORDS

EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.

REFERENCE

1 (bases 1 to 800)
 Buerstedde, J.M.
 Gallus gallus bursa lymphocyte EST
 Unpublished (2002)
 Contact: Buerstedde JM
 Cellular Immunology
 Heinrich-Pette-Institute
 Martinstr. 52, 20251 Hamburg, Germany
 Email: <http://genetics.hpi.uni-hamburg.de/dc40est.html>.

FEATURES

source

1. 800
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /db_xref="taxon:9031"
 /clone="3d2082"
 /cell_type="bursal lymphocyte"
 /dev_stage="2-3 weeks old"

ORIGIN /clone_11b="r1ken1"
/note="TCB indred strain"

Alignment Scores:

Pred. No.:	8.82e-97	Length:	800
Score:	1335.00	Matches:	241
Percent Similarity:	93.6%	Conservative:	8
Best Local Similarity:	90.6%	Mismatches:	17
Query Match:	35.2%	Indels:	1
DB:	1	Gaps:	0

US-10-755-889-18 (1-706) x AJ454603 (1-800)

```
QY 438 SerThrIleProGlnAlaSerArgLeuAsnIleValAsnArgSerMetThrGlySer 457
    |||||
DB 798 TCCAAATATCCCGCAAGGAGAGAGACTCAACAACATTGTAAACAGTCGCGGATGGGCTCC 739

QY 458 ProArgSerSerSerGluSerHisSerProLeuThrMetHisProProGlyGlyThrSer 477
    |||||
DB 738 CCGGCGCAA-GCAAGTGAAGGGGAGGAGTCCCGCTCTACATGATGAAAGTGCAGCTCC 680

QY 478 CygSglSerGlnSerProGlnHisAlaGluMetCysLeuHisThrAlaGlyProThrPhe 497
    |||||
DB 679 TGGGAGTCCAGTCCCGGCAACACATTGAGATGAGCTTCAACCTCTGGCTCAGCCTTT 620

QY 498 AlaGluGluMetGlyGluThrGlnSerGlyThrSerAspSerSerCysGluAsnGlyAla 517
    |||||
DB 619 GGAAGAAAGATGGGGGAAACCCAGTCTGAGTACTGACTCAGNTGGAGAAACGAGACC 560

QY 518 PhePheCysAsnGluCysAspCysArgPheSerGluGluAlaSerLeuValArgHisThr 537
    |||||
DB 559 TTCTTCTGCAACGAGTGTGACTGCCGGTCTCCAGAGGCGCTCGCTCAAGAGGCACTCT 500

QY 538 LeuGlnThrHisSerAspLeuProGlyCysAspArgCysGlnAlaSerPheArgTyr 557
    |||||
DB 499 CTGCAAGTCCACACGACAAACCTTACAGTGCACGCTGCAGGCTCTCTCGCTAC 440

QY 558 LysGlyAsnLeuAlaSerHisValThrValHisThrGlyGlyLeuProGlyArgCysAsn 577
    |||||
DB 439 AAGGGGAACCTCCGCAAGCACAACACCTCCACACAGAGAAAGCCGTCACGCTGCAC 380

QY 578 IleCysGlyAlaGlnPheAsnArgProAlaAsnLeuValHisThrHisThrArgHisSer 597
    |||||
DB 379 ATCTGTGGGGCGGAGTTCACCGGCGCAGCCCAACCTGAAACCCACACACGTAATTCACCTCC 320

QY 598 GlyGlyLeuProGlyArgCysGluThrCysGlyAlaArgPheValGlnValHisSer 617
    |||||
DB 319 GGAAGAAAGATGGGGGAAACCCAGTCTGAGTACTGACTCAGNTGGAGAAACGAGACC 260

QY 618 ArgAlaHisValLeuIleHisThrGlyGlyLeuProGlyArgCysGlyThr 637
    |||||
DB 259 CGTGTCTATGTGCTCATTCATCTGAGGAGAAAGCCATCCCTGAGATCTGTGCGACA 200

QY 638 ArgPheArgHisValLeuGlnThrLeuValSerHisLeuArgHisThrGlyGlyLeuPro 657
    |||||
DB 199 CGTTTCCGCGCACTGCAACACCTCAAAAGCCACTTGCATTCACACGCGGCGAGAAACCT 140

QY 658 TyrHisCysGlyGlyLeuValAsnLeuHisPheArgHisValSerGlnLeuArgLeuHisSer 677
    |||||
DB 139 TATCATTTGTGAGAAATGCAACTGCACTTCGCGCAAAAGCCAGCTCGGCTGCACCTG 80

QY 678 ArgGlnValHisValAlaIleThrAsnThrValGlnTyrArgValSerAlaThrAsp 697
    |||||
DB 79 CGGCAAGAAAGCAGGGGCCATCAACAACAGAGTCAAGTACCGCATCTCGGCGCAACGAG 20

QY 698 LeuProProGluLeuPro 703
    |||||
DB 19 GTGCTCCGAGACTCCCC 2

RESULT 13
BQ716058 804 bp mRNA linear EST 16-JUL-2002
LOCUS
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DEFINITION AGENCOURT 8103534 lupski sympathetic_trunk Homo sapiens cDNA clone
IMAGE:6190896 5', mRNA sequence.

ACCESSION BQ716058
VERSION BQ716058.1 GI:21854955
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 804)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
<http://image.llnl.gov>
Plate: LHAM3590 row: h column: 01
High quality sequence stop: 688.

FEATURES
Location/Qualifiers
1..804
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6190896"
/sex="male"
/tissue_type="sympathetic trunk"
/dev_stage="adult, 16 yr"
/lab_host="DH10B"
/note="Vector: pCMV-SPORE6 (Life Technologies); Site_1:
/clone_11b="lupski sympathetic trunk"
NOTI; Site 2: SalI, cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCAGCGTCCG-3' and
5'-GACTAGTTCTAGATCCGAGCGGCGCTT(15)-3'. Size selected >
1 kb for average insert length 1.9 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine); available through Life
Technologies."

ORIGIN

Alignment Scores:

Pred. No.:	1.7e-96	Length:	804
Score:	1331.50	Matches:	260
Percent Similarity:	97.4%	Conservative:	0
Best Local Similarity:	97.4%	Mismatches:	6
Query Match:	35.1%	Indels:	1
DB:	5	Gaps:	1

US-10-755-889-18 (1-706) x BQ716058 (1-804)

```
QY 21 AsnLeuAsnArgLeuAspSerArgAspIleLeuThrAspValValIleValSerArg 40
    |||||
DB 3 AACCTTAATGCTCTCCGAGTCCGAGACATCTTGAATGATGTGTGATGAGCGCT 62

QY 41 GluGlnPheArgAlaHisValThrValLeuMetAlaCysSerGlyLeuPheTyrSerIle 60
    |||||
DB 63 GAGCAGTTTAGAGCCATAAAGCGTCTCATGCGCTGCAGTGCCTGTTCTATAGCATC 122

QY 61 PheThrArgGlnLeuValCysAsnLeuSerValIleAsnLeuAspProGluIleAsnPro 80
    |||||
DB 123 TTTCAGACCAAGTTGAATGCAACTTAGTGTGATCAATCTGAGATCAACCTT 182

QY 81 GluGlyPheCysIleLeuLeuAspPheMetTyrThrSerArgLeuAsnLeuArgGluGly 100
    |||||
DB 183 GAGGGAATTCGATCTCTGACTTCATGTACACATCTGGGCTCAATTTGGGAGAGGC 242
```

QY 101 AenlllMeetAlaValMetAlaThrAlaMetYrleuGluMetGluHlsValAlaPThr 120
Db 243 AACATATGAGCTGTGTATGGCAAGGCTATGTAACCTCAATGAGATGTTGGACACT 302
QY 121 CyArGLySPheIlleYsAlaSerGluAlaGluMetValSerAlaIleYsProProArg 140
Db 303 TGGCGGAAGTTTATTAAAGCCAGTAAAGCAGATGTTTCTGCCATCAAGCCTCTCGT 362
QY 141 GluGluPheLeuAunSerArgMetLeuMetProGluAspIleMetAlaTyrArgGlyArg 160
Db 363 GAAGAGTTCTCTCAACAGCCGAGTGTGATGCCCCAAGACATCATGCGGCTCGT 422
QY 161 GluValValGluAunAunLeuProLeuAysSerAlaProGlyCySGluSerArgAlaPhe 180
Db 423 GAAGTGTGAGAAACAACCTGCACTGAGAGAGCCCTGGGTGTAGAGCAGAGCCTTT 482
QY 181 AlaProSerLeuTyrSerGlyLeuSerThrProProAlaSerTyrSerMetTyrSerHis 200
Db 483 GCCCCAGAGCTGTACAGTGGCTGTTCACACCGCCAGCCTTTATTCATGTACAGCCAG 542
QY 201 LeuProValSerSerLeuLeuPheSerAspGluGluPheArgAspValArgMetProVal 220
Db 543 CTCCTGTCAGACAGCTCTCTCTTCGATGAGAGATTCGAGATGTCGAGATGCTGTG 602
QY 221 AlaAsnProPheProGlyGluArgAlaLeuProCyAsnSerAlaArgProValProGly 240
Db 603 GCCAACCCCTTCCCAAGAGGAGGCACTCCCATGTATGTGTCAGGCGAGTCCCTGGT 662
QY 241 GluTyrSerArgProThrLeuGluValSerProAsnValCyHisSerAsnIleTyrSer 260
Db 663 GAGTACAGCGCGCGAGCTTTGAGAGTGTCCCAATGTGTGCCAGCATATATCTATTCA 722
QY 261 ProGlyGluThrIleProGluGluAlaArgSerAspMetHisTyrSerValAla---Glu 279
Db 723 CCCAAAGAAACAATCCAGAAAGAGGACAGAAATGATATGACATACGTGTGGCTGAG 782
QY 280 GlyLeuLysProAlaAlaPro 286
Db 783 GCCCTCAACCTCTGCTGCCCC 803

RESULT 14
BX419860 849 bp mRNA linear EST 01-MAY-2004
LOCUS BX419860 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
DEFINITION CS0DF021YF19 5-PRIME, mRNA sequence.
ACCESSION BX419860
VERSION BX419860.2 GI:46925086
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 849)
I.J.W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30638052.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-Oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 2184.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?us=CS0DF021CC100P1ac=2184.r.
FEATURES
Location/Qualifiers
1..849

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DF021YF19"
/librase_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-Oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

ORIGIN

Alignment Scores:
Pred. No.: 8,4e-93 Length: 849
Score: 1286.00 Matches: 250
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 33.9% Indels: 0
DB: 5 Gaps: 0

US-10-755-889-18 (1-706) x BX419860 (1-849)

QY 1 MetAlaSerProAlaAspSerCysIleGluPheThrArgHisAlaSerAspValLeu 20
Db 100 ATGGCTCGCGGCTGACAGCTGTATCCAGTTACACCGCCATGCCAGATGTTCTTCTC 159
QY 21 AenLeuAunAunGluAysSerArgAspIleLeuThrAspValIleValValSerArg 40
Db 160 AACCTTAATCGTCTCCGAGTGCAGACATCTTGACTGATGTTGTATTGTGAGCCGT 219
QY 41 GluGluPheArgAlaHisIleThrValIleuMetAlaCysSerGlyLeuPheTyrSerIle 60
Db 220 GAGCAGTTTAAAGCCCATTAACGGTCTTCATGCTGCTGAGCTGCTGTTCTTATGATC 279
QY 61 PheThrAspGluLeuLysCysAsnLeuSerValIleAsnLeuAspProGluIleAsnPro 80
Db 280 TTTCAGACACCACTTGAATGAACCTTAGTGATGATCAATCTGATCTTGATCAACCT 339
QY 81 GluGlyPheCysIleLeuLeuAspPheMetYrThrSerArgLeuAunLeuArgGly 100
Db 340 GAGGATCTGTCATCTCTCTGACATTCATGACATCTCGGCTCAATTTGGGAGAGGC 399
QY 101 AenlllMeetAlaValMetAlaThrAlaMetYrleuGluMetGluHlsValAlaPThr 120
Db 400 AACATATGAGCTGTGTATGGCAAGGCTATGTAACCTCAATGAGATGTTGGACACT 459
QY 121 CyArGLySPheIlleYsAlaSerGluAlaGluMetValSerAlaIleYsProProArg 140
Db 460 TGGCGGAAGTTTATTAAAGCCAGTAAAGCAGATGTTTCTGCCATCAAGCCTCTCGT 519
QY 141 GluGluPheLeuAunSerArgMetLeuMetProGluAspIleMetAlaTyrArgGlyArg 160
Db 520 GAAGAGTTCTCTCAACAGCCGAGTGTGATGCCCCAAGACATCATGCGGCTCGT 579
QY 161 GluValValGluAunAunLeuProLeuAysSerAlaProGlyCySGluSerArgAlaPhe 180
Db 580 GAAGTGTGAGAAACAACCTGCACTGAGAGAGCCCTGGGTGTAGAGCAGAGCCTTT 639
QY 181 AlaProSerLeuTyrSerGlyLeuSerThrProProAlaSerTyrSerMetTyrSerHis 200
Db 640 GCCCCAGAGCTGTACAGTGGCTGTTCACACCGCCAGCCTTTATTCATGTACAGCCAG 699
QY 201 LeuProValSerSerLeuLeuPheSerAspGluGluPheArgAspValArgMetProVal 220
Db 700 CTCCTGTCAGACAGCTCTCTTCTCCGATGAGAGTTCGGGATGTCCGAGTGCCTGTG 759
QY 221 AlaAsnProPheProGlyGluArgAlaLeuProCyAsnSerAlaArgProValProGly 240
Db 760 GCCAACCCCTTCCCAAGAGGAGGCACTCCATGTATGTGCCAGGCGAGTCCCTGGT 819
QY 241 GluTyrSerArgProThrLeuGluValSer 250

Db 820 GAGTACGCGCCGACCTTGAAGTGTCC 849

RESULT 15
AJ441866 798 bp mRNA linear EST 19-Apr-2002
DEFINITION AJ441866 dkfz426 Gallus gallus CDNA clone 14a20r1, mRNA sequence.
ACCESSION AJ441866
VERSION AJ441866.1 GI:20209087
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Bukarvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archaeoptera; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 798)
Buerstedde, J.M.
REFERENCE Buerstedde, J.M.
AUTHORS Gallus gallus bursal lymphocyte EST
TITLE Unpublished (2002)
JOURNAL Contact: Buerstedde JM
COMMENT Cellular Immunology
Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: <http://genetics.mpi.uni-hamburg.de/dt40est.html>.
Location/Qualifiers
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/dev_stage="2-3 weeks old"
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FEATURES
source

ORIGIN

Alignment Scores:
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Percent Similarity: 96.2% Conservative: 6
Best Local Similarity: 93.8% Mismatches: 9
Query Match: 33.9% Indels: 0
DB: 1 Gaps: 0

US-10-755-889-18 (1-706) x AJ441866 (1-798)

QY 467 ProLeuTyMeThiSPProLySCyThSerCySGLySerGlnSerProGlnHisAla 486
Db 1 CCGCTCTCATGATTCATTCGAAGTGCAGTCTGCGGCTGCCAGTCCCCCAACACACT 60
QY 487 GlnMetCysLeuHisThiAlaGlyProThrPheAlaGlnGlnMetGlyGlnThrGlnSer 506
Db 61 GAGATGTGCTTCACACTCTGCTGACCTTTGAGAGAGATGGGGAACCAAGTCT 120
QY 507 GlnTySerAspSerSerCysGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 526
Db 121 GAGTACTTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 527 PheSerGlnGlnAlaSerLeuHisThiAlaGlnGlnGlnGlnGlnGlnGlnGlnGln 546
Db 181 TTCTCCGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 547 LysCysAspArgCysGlnAlaSerPheArgTyrLysGlnAlaSerHisIleThr 566
Db 241 AAGTGCAGCCGTGCAAGCTCTTCGCTACCAAGGCACTGCTGCTGCTGCTGCTGCTGCT 300
QY 567 ValHisThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 586
Db 301 GTCCACACAGAGAAAGCCGTCGCAACATCTGTGGGCGCAGTTCAACCGGCA 360
QY 587 AlaLeuLeuTyThiHisThrArgLysHisSerGlnGlnGlnGlnGlnGlnGlnGlnGln 606

Db 361 GCCAAGCTGAAACCCACACAGTATTCATCTCCGAGAGAAACCTTACAGTGCAGACC 420
QY 607 CysGlyAlaArgPheValGlnValAlaHisIleLeuArgAlaHisValLeuHisThiGly 626
Db 421 TGTGGGGCCAGATTGTTCAGAGTGGCCACCTCGTCTCATGTGCATTCATTCAGTGGG 480
QY 627 GlnTyProTyProCysGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 646
Db 481 GAGAGGCAATACCCCTGTGAGATCTGTGGACACGTTTCCGCACTGCGACACCTCAAA 540
QY 647 SerHisLeuArgLysHisThiGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 666
Db 541 AGCCACTTGCATTCACACAGGCGAGAACTTATCATTTGTGAAGTGCACACTGCAC 600
QY 667 PheArgHisIleSerGlnLeuAlaGlnLeuHisIleLeuArgGlnGlnGlnGlnGln 686
Db 601 TTCGGCCACAAAGCCAGCTGCGGCTGCACCTGCGGCAAGACACGGGGCCATCACAAAC 660
QY 687 ThrTyValGlnTyArgValSerAlaThrAspLeuProGlnLeuProGlnAlaCys 706
Db 661 ACCAAGGTGAGTACGCAATCTGCGCAACGAGGTGCTCCGAGCTCCCAAGGCTTTC 720

Search completed: March 2, 2006, 02:23:41
Job time : 4896 secs

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GenCore version 5.1.7
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CM protein - nucleic search, using frame_plus.p2n model

Run on: March 2, 2006, 01:02:20 ; Search time 336 Seconds
(without alignments)
3734.996 Million cell updates/sec

Title: US-10-755-889-18

Perfect score: 3793

Sequence: 1 MASPDSCIQFTRHASDVL.....TKVQVRSATDLPPELPKAC 706

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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5	3763	99.2	3720	3	US-09-268-202-1
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7	3763	99.2	3720	6	PCR-US94-06669-1
8	621.5	16.4	2769	3	US-09-620-312D-309
9	614.5	16.2	2680	3	US-09-063-035-1

10	540	14.2	2289	3	US-09-949-016-1780	Sequence 1780, Ap
11	508	13.4	2184	3	US-09-949-016-4402	Sequence 4402, Ap
12	503	13.3	3052	3	US-10-104-047-959	Sequence 959, App
13	500	13.2	2920	3	US-09-620-312D-1084	Sequence 1084, Ap
14	498.5	13.1	2948	3	US-09-774-528-145	Sequence 145, App
15	498.5	13.1	2948	3	US-10-120-988-145	Sequence 145, App
16	495	13.1	2320	3	US-09-016-434-1054	Sequence 1054, Ap
17	491	12.9	1892	2	US-08-933-750C-66	Sequence 66, Appl
18	491	12.9	1892	3	US-09-234-613-66	Sequence 66, Appl
19	489	12.9	2441	3	US-09-949-016-2756	Sequence 2756, Ap
20	483.5	12.7	3798	3	US-09-949-016-4204	Sequence 4204, Ap
21	482.5	12.7	3839	3	US-09-949-016-485	Sequence 485, App
22	482.5	12.7	156942	3	US-09-949-016-15946	Sequence 12227, A
23	482.5	12.7	156942	3	US-09-949-016-15946	Sequence 15946, A
24	482	12.7	19861	3	US-09-949-016-14498	Sequence 14498, A
25	480	12.7	2555	3	US-09-620-312D-1050	Sequence 1050, Ap
26	477	12.6	2804	3	US-09-949-016-14204	Sequence 2278, Ap
27	477	12.6	22294	3	US-09-949-016-14202	Sequence 14202, A
28	475.5	12.5	3252	3	US-09-774-528-104	Sequence 104, App
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30	474.5	12.5	2784	3	US-10-104-047-1944	Sequence 1944, Ap
31	473	12.5	3090	3	US-10-104-047-191	Sequence 191, App
32	470.5	12.4	2771	3	US-09-976-594-691	Sequence 691, App
33	469.5	12.4	2925	3	US-09-620-312D-163	Sequence 163, App
34	468.5	12.4	2110	3	US-10-104-047-1778	Sequence 1778, Ap
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37	465	12.3	3240	3	US-09-949-016-5548	Sequence 5548, App
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39	464.5	12.2	27227	3	US-09-949-016-17365	Sequence 17365, A
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43	462.5	12.2	2634	3	US-10-104-047-816	Sequence 816, App
44	461.5	12.2	1833	3	US-10-104-047-1491	Sequence 1491, App
45	461	12.2	2351	3	US-09-016-434-1337	Sequence 1337, Ap

ALIGNMENTS

RESULT 1
US-09-418-640-3
Sequence 3, Application US/09418640
Patent No. 6140125
GENERAL INFORMATION:
APPLICANT: Jennifer K. Taylor
TITLE OF INVENTION: ANTISENSE MODULATION OF BCL-6 EXPRESSION
FILE REFERENCE: RRS-0102
CURRENT APPLICATION NUMBER: US/09/418, 640
CURRENT FILING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 3
LENGTH: 3536
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: CDS
LOCATION: (328)..
US-09-418-640-3

Alignment Scores:

Pred. No.: 2.45e-279
Score: 3793.00
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
DB: 3
Gaps: 0

US-10-755-889-18 (1-706) x US-09-418-640-3 (1-3536)

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|||||


```

GENERAL INFORMATION:
APPLICANT: Horwitz, Kathryn
TITLE OF INVENTION: Progesterone Receptor-Regulated Gene Expression and Methods Relat
FILE REFERENCE: 2848-39
CURRENT APPLICATION NUMBER: US/09/814,915A
CURRENT FILING DATE: 2002-03-21
PRIORITY APPLICATION NUMBER: 60/214,870
PRIORITY FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PatentIn version 3.1
SEQ ID NO 90
LENGTH: 3536
TYPE: DNA
ORGANISM: Homo sapiens
US-09-814-915A-90

Alignment Scores:
Pred. No.: 2,456-279 Length: 3536
Score: 3793.00 Matches: 706
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US-10-755-889-18 (1-706) x US-09-814-915A-90 (1-3536)

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QY 461 SerSerGlnSerHisSerProLeuTyrMetHisProProLysCysThrSerCysGlySer 480
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QY 521 AsnGlyCysAspCysArgPheSerGlnGlnAlaSerLeuLysAspGlnHisThrLeuGlnThr 540
DB 1888 AATGAGTGTGATCCCGTCTCTGAGAGAGGCTTCACTCAAGAGAGACACACCTGAGACC 1947
QY 541 HisSerAspLysProTyrLysCysAspArgCysGlnAlaSerPheArgTyrLysGlyAsn 560
DB 1948 CACGTGACAAACCTTACATGATGTGACCGCTGCAAGGCTCTCTTCCGTTACAGAGGCAAC 2007
QY 561 LeuAlaSerHisLysThrValHisThrGlyGlnLysProTyrArgCysAsnIleCysGly 580
DB 2008 CTCGCGACGACCAAGACCGTCCATACCGGTGAGAAACCTTATCTGTCGACAAATCTGTGG 2067
QY 581 AlaGlnPheAsnArgProAlaAsnLeuLysThrHisThrArgIleHisSerGlyGlnLys 600

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Qy 601 ProTyrIlyeCysegluThrCyseglYAlaHqPheValGlnValAlaHisleuAlaHis 620
Db 2128 CCTCAAAAGCCAAACCTGCGAGCACTGATGTCAGTGGCCCACTCCCTGCAT 2187
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Qy 701 GluleuProlysaIaCyse 706
Db 2428 GAGCTCCCAAGCTTC 2445

RESULT 3
US-08-074-967-1
Sequence 1, Application US/08074967
Patent No. 5641672
GENERAL INFORMATION:
APPLICANT: Dalla-Favera, Riccardo
APPLICANT: Chasanti, R.S.K.
TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS
TITLE OF INVENTION: bcl-6
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/074,967
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/43771
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3720 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
NAME/KEY: CDS
LOCATION: 328..2445
US-08-074-967-1

Alignment Scores:

	Pred. No.:	5,12e-277	Length:	3720
Score:		3763.00	Match:	701
Percent Similarity:		99.4%	Conservative:	1
Best Local Similarity:		99.3%	Mismatches:	4
Query Match:		99.2%	Indels:	0
DB:		2	Gaps:	0

US-10-755-889-18 (1-706) x US-08-074-967-1 (1-3720)

Qy 1 MetAlaSerProAlaAspSerCyseIleGlnPheThraArgHisAlaSerAspValleu 20
Db 328 ATGGCTTCGCGCGCTGACAGCTGTATCCAGTACCCCGCAAGGAGATGTTCTTC 387
Qy 21 AsnleuAsnArgleuAsnSerArgAspIleleuThraAspValIleValIaSerArg 40
Db 388 AACCTTAATGCTCTCCGAGTGAAGACATCTTGATGATGTTGTATCTTGTGAGCCT 447
Qy 41 GluIlnPheArgAlaHisIlyeThraIleuMetAlaCyseSerGlyleuPheTyrSerIle 60
Db 448 GAGCATTTAGAGCCCATTAACGGTCCATGCGCTGGAGAGGCTGTTATAGCATC 507
Qy 61 PheThraPheGlnleuLysCyseAnleuSerValIleAsnleuAspProGluIlnleuPro 80
Db 508 TTACAGACCAAGTGAATGCAACCTTAGTGAATCAATGATCTGAGATCAACCT 567
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Db 568 GAGGATTTCTGATCTCTCTGACATTCATGACATCTCGGCTCATTTGGGAGAGGC 627
Qy 101 AsnIleMetAlaValMetAlaThraIleuTyrleuGlnMetGluHisValIaPheThr 120
Db 628 AACATCATGCTGTGATGAGCCAGCGCTATGATCTGAGATGAGCATGTTGTGACACT 687
Qy 121 CyseArgLysPheIleValIaSerGluAlaGlnMetValSerAlaIleIlyePheProArg 140
Db 688 TGCCGGAATTAATTAAGCCAGTGAAGCAAGATGTTCTGCCATCAAGCTCTCTCT 747
Qy 141 GluGluPheleuAsnSerArgMetleuMetProGlnAspIleMetAlaTyrArgGlyArg 160
Db 748 GAGAGATTCCTCAACGCCGAGTGTGATGCCCAAGACATCATGCGGATCGCT 807
Qy 161 GluValIaGluAsnAsnleuProleuArgSerAlaProGlyCyseGlnSerArgAlaPhe 180
Db 808 GAGTGTGTGAGAACCACTGCACTGAGAGAGCGCCCTGGAGTGTAGAGAGAGCTTT 867
Qy 181 AlaProSerleuTyrSerGlyleuSerThrProProAlaSerTyrSerMetTyrSerHis 200
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Qy 201 leuProValSerSerleuPheSerArgGluGluPheArgAspValArgMetProVal 220
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Qy 221 AlaAsnProPheProlysgluArgAlaIleuProCyseAspSerAlaArgProValProGly 240
Db 988 GCCAACCTTCCCAAGAGAGGCGGACCTCCATGTATGTGCCAGGCCAGTCCCTGAT 1047
Qy 241 GluTyrSerArgProThrluGlnIleuLysSerProAsnValCyseHisSerAsnIleTyrSer 260
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Qy 301 LysGluGluGluArgProSerSerGluAspGluIleAlaIleuHsthPheGluProProAn 320
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US-08-553-541B-1

; Patent No. 5882858

APPLICANT: Dalla-

TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS

NUMBER OF SEQUENCES: 9

ADDRESSEE: Cooper & Dunham LLP

CITY: New York

COUNTRY: United States of America

COMPUTER READ ;

COMPUTER:

SOFTWARE: PatentIn Release #1.0, Version #1.25

APPLICATION NUMBER: US/08/553,541B

CLASSIFICATION: 435

NAME: White, John P.

REFERENCE/DOCKET NUMBER: 0575/43771-A-PCT-US

TELEPHONE: (212) 278-0400

TELEX: 422523 COOP UI

SEQUENCE CHARACTERISTICS:

TYPE: nucleic acid

TOPOLOGY: linear

FEATURE:

LOCATION: 328..2445

Pred. No.:

Percent Similarity

Query Match:

100-443887-1 (1-3720)

[illegible]

38

01 1ast author not author of author [Val]T [Leva]Val] SerArg 40

[illegible]

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100

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 Db 508 TTATACAGACCAAGTTGAATGCACCTTAGTGTATCATATTAGATCTTGAGATCAACCTT 567
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 Db 568 GAGGAGATTTCGATCCCTCGATCTTCATGTACACATCTCGCTCAATTGGCGGAGGGC 627
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 Db 628 AACATCATGGCTGTGTATGGCAGCGCTATGTACTCTCAGATGAGAGATGTGTGGACACT 687
 Qy CysArgLysPheIleLeuValSerGluAlaGluMetValSerAlaIleLeuSerProArg 140
 Db 688 TGGCGGAAGTTTATTAAAGCCAGTGAAGCAGAGATGGTTTCTGCCATCAAGCTCTCTCGT 747
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 Db 748 GAAGAGTTCTTCAACAGCCGGATGTGATGCCCCAAGACATCATGGCTTATGGGGTCCGT 807
 Qy GluValValGluAsnAsnLeuProLeuArgSerAlaProGlyCysGluSerArgAlaPhe 180
 Db 808 GAGGTGTGAGAAACAACCTGCACTGAGAGAGCGCCCTGGGTGTGAGACAGACGCTTT 867
 Qy AlaProSerLeuTyrSerGlyLeuSerThrProProAlaSerTyrSerMetTyrSerHis 200
 Db 868 GCCCCAGCCTGTACATGGCTGTGTCCACACCGCAGCCTTATTCACATGACAGCAC 927
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 Db 988 GCCAACCCCTTCCCAAGAGAGCGGCGCACTCCCATGTATGTATGTCCAGGCGACGCTCCGT 1047
 Qy GluTyrSerArgProThrLeuGluValSerProAsnValCysHisSerAsnIleTyrSer 260
 Db 1048 GAGTACAGCGCGCGCATTTGAGAGTGTCCCCCATGTGTGCGCACACCAATATCTATTCA 1107
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 Qy LeuLeuProAlaAlaProSerAlaArgAsnAlaProTyrPheProCysAspValAspSer 300
 Db 1168 CTCAAACCTGCTGCCCCCTCAGCCCGAAATGCCCCCTACTTCTGTGACAAAGGCGCAGC 1227
 Qy LysGluGluGluArgProSerSerSerGluAspGluIleAlaLeuHisPheGluProProAsn 320
 Db 1228 AAAGAAAGAGAGAACCTCTCTCGAAGATGAGATTCCTGCAATTCGAGCCCCCAAT 1287
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 Db 1288 GCACCCCTGAAGCGGAGGCTGTGTATGTCCACAGAGCCCCCAAGAAATGATGCTGCGAG 1347
 Qy ProAsnSerProThrGluAlaCysSerSerIleAsnAlaCysIleLeuGlnAlaSerGly 360
 Db 1348 CCCAACTCGCCCAAGAGCGCTGCAAGATGAAGATCTTCGACAGGGGTTCGCG 1407
 Qy SerProProAlaLysSerProThrAspProLysAlaCysAsnTrpLysIleTyrLysPhe 380
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 Db 1528 GGCGGCTTTCCTCCAGAGGCTTACAGCGGCCCACTGCTGTGCGAGCCACCATGAGACCT 1587

Qy 421 GluAsnLeuAspLeuGlnSerProThrLysLeuSerAlaSerGlyGluAspSerThrIle 440
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 Qy 441 ProGlnAlaSerArgLeuAsnAsnIleValAsnArgSerMetThrGlySerProArgSer 460
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 Qy 461 SerSerGluSerHisSerProLeuTyrMetHisProProLysCysThrSerCysGlySer 480
 Db 1708 AGCAGCGAGGCACTTACCACTTACATGACCCCCCGAAGTGCAGCTTCGGGGCTT 1767
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 Db 1768 CAGTCCCAACAGACATGACAGATGTGCTCCACACCGCTGGCCCCACGTCCTGAGAG 1827
 Qy 501 MetGlyGluThrGlnSerGluTyrSerAspSerSerCysGluAsnGlyAlaPheMetCys 520
 Db 1828 ATGGGAGAGAACCCAGCTGAGTACTCAGATTCAGATCTGTGAGAAAGGGGCTTCTTTCG 1887
 Qy 521 AsnGluCysAspCysArgPheSerGluGluAlaSerLeuLysArgHisThrLeuGlnThr 540
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 Qy 541 HisSerAspLysProTyrLysCysAspArgCysGlnAlaSerPheArgTyrLysGlyAsn 560
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 Qy 561 LeuAlaSerHisLysThrValHisThrGlyGlyLysProTyrArgCysAsnIleCysGly 580
 Db 2008 CTCGCGAGCACAAGACCTCCATACCGGTGAGAAACCTATCGTTGCAACATCTGTGG 2067
 Qy 581 AlaGlnPheAsnArgProAlaAsnLeuSerThrHisThrArgIleHisSerGlyGlyLys 600
 Db 2068 GCCAGTTAAACGGCGACCCAACTTGAAACCACACTCGAATTCATCTTGAGAGAGAG 2127
 Qy 601 ProTyrLysCysGluThrCysGlyAlaArgPheValGlnValAlaHisLeuArgAlaHis 620
 Db 2128 CCTCAAAATGGGAAACCTGCGGAGCAGATTTGTATCAGTGTGCGCACCTCGTGCCAT 2187
 Qy 621 ValLeuIleHisThrGlyGlyLysProTyrProCysGluIleCysGlyThrArgPheArg 640
 Db 2188 GTGCTTATCAACACTGTGTAGAGCCCTATCCCTGTGAAATGTGTGGCACCGGTTCGCG 2247
 Qy 641 HisLeuGlnThrLeuLysSerHisLeuArgIleHisThrGlyGlyLysProTyrHisCys 660
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 Db 2308 GAGAACTGTAACTGATTCGCTGCACAAAGCAGCTGCACTTGGCGCGAGAG 2367
 Qy 681 HisGlyAlaIleThrAsnThrLysValGlnTyrArgValSerAlaThrAspLeuProPro 700
 Db 2368 CATGGCGCATCAACCAACCAAGGTGCAATACCGGTGTGAGCCACTGACCTGCTCG 2427
 Qy 701 GluLeuProLysAlaCys 706
 Db 2428 GAGCTCCCAAGCCTGCG 2445

RESULT 5
 US-09-268-202-1
 ; Sequence 1, Application US/09268202
 ; Patent No. 6174997
 ; GENERAL INFORMATION:
 ; APPLICANT: Dalia-Favera, Riccardo
 ; APPLICANT: Chaganti, Raju S.K.
 ; TITLE OF INVENTION: CLOTHING AND USES OF THE GENETIC LOCUS
 ; TITLE OF INVENTION: bcl-6
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/268,202
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/43771-A-PCT-US-2
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3720 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 328..2445.
US-09-268-202-1

Alignment Scores:
Pred. No.: 5.12e-277 Length: 3720
Score: 3763.00 Matches: 701
Percent Similarity: 99.4% Conservative: 1
Best Local Similarity: 99.3% Mismatches: 4
Query Match: 99.2% Indels: 0
Gaps: 0
US-10-755-889-18 (1-706) x US-09-268-202-1 (1-3720)
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QY 21 AsnLeuAsnArgLeuArgSerArgAspIleLeuThrAspValIleValIleValSerArg 40
DB 388 AACCTTATGCTCTCCGAGTCCGAGATCGAGACATCTTGACTGATGTTGTCATGTTGAGCCGT 447
QY 41 GluGlnPheArgAlaHisIleValThrValIleuMetAlaCysSerGlyLeuPheTyrSerIle 60
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DB 508 TTTCAGACGAGTTGAAATGCACTTATGTGTATCATCTAGATCTTCAATCAACCTT 567
QY 81 GluGlyPheCysIleLeuLeuAspPheMetTyrThrSerArgLeuAsnLeuArgGly 100
DB 568 GAGGAGTTCTGCACTCTCTCGAGACTTCATGATACATCTCGGCTCAATTTCCGGAGAGGC 627
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DB 628 AACATCATGCTGTGATGCGCAGCGCTATGTACCTGAGATGAGACATGTTGTGAGCACT 687
QY 121 CysArgLysPheIleValAlaSerGlnIleGlnMetValSerAlaIleValProProArg 140
DB 688 TGCCGGAAGTTTATTAAAGCCAGTGAAGCAAGATGTTTCTGCAATCAAGCTCTCTCTGT 747
QY 141 GluGlnPheLeuAsnSerArgMetLeuMetProGlnAspIleMetAlaTyrArgGlyArg 160

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DB 808 GAGGTGTGTGAAGAACCACTGCGCATGAGAGGCCCTGAGTGTAGAGCAAGACCTTT 867
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DB 1108 CCAAGAGAACATCCCAAGAGGCAAGAGATGTATGACATCACTGCTGAGGCGC 1167
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DB 1168 CTCAACTGTCTCCCTCAGGCCGGAATGCCCTTACTTCTGTGCAAGGCGCAGC 1227
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DB 1648 CCAACACCCGCGCTCAATACATGTTTAAAGTTCATGACAGAGGCTCTCCCGGAGGC 1707
QY 461 SerSerGluSerHisSerProLeuTyrMetHisProProLysCysThrSerCysGlySer 480
DB 1708 AGCAGCAGAGCACTACCACTTATACATCAACCCCGAAGTGCAGTCTGCGGCTCT 1767
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QY 241 GluTyrSerArgProThrLeuGluValSerProAsnValCysHisSerAsnIleTyrSer 260
 DB 1048 GAGTACGCGCGCGGCGATTTGGAGGTGTCCCGCAATGTGGCCACACCAATCTATCTTCA 1107
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 QY 281 LeuLysProAlaAlaProSerAlaArgAsnAlaProTyrPheProCysAspLysAlaSer 300
 DB 1168 CTCAAACTCTGCTGCTCCCTCAGCGCCGAATGCCCTTACTTCCCTTGTGACAGGGCAGC 1227
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 DB 1228 AAGAAGAGAGAGAGACCTCTCGAAGATGAGATTCCTCGCATTTTCGAGCCCCCAAT 1287
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 DB 1528 GGGCGGCTTTTCCACAGGCTTACAGGCGCCCACTGCTGCTGCGACCCATGAGGCT 1587
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 QY 441 ProGlnAlaSerArgLeuAsnAsnIleValAsnArgSerMetThrGlySerProArgSer 460
 DB 1648 CCACAGCGCAGCCGCTCAATACATCTTAAACAGGTCTCAGACGGGCTCTCCCGCAGC 1707
 QY 461 SerSerGluSerHisSerProLeuTyrMetHisProProLysCysThrSerCysGlySer 480
 DB 1708 AGCAGCGAGAGCCCACTCACTCACTACATGCAACCCCGAAGTGACGCTCGGGCTCT 1767
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 DB 1768 CAGTCCCGCAGCATGCGAGATGTGCTCCACACCGCTGCGCCACGTTGCTGAGAGAG 1827
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 DB 1828 ATGGAGAGAGACCCAGTCTGAGTACTCAGATTCTAGCTGTGAGACGGGGCTTCTTCTGC 1887
 QY 521 AsnGluCysAspCysArgPheSerGluGluAlaSerLeuLysArgHisThrLeuGlnThr 540
 DB 1888 AATGAGTGTGACTGCGCTTCTCTAGAGAGGCTCTACAGAGGACACCGCTGAGACC 1947
 QY 541 HisSerAspLysProTyrLysCysAspArgCysGlnAlaSerPheArgTyrLysGlyAsn 560
 DB 1948 CACAGTGCACAAACCTTACAGTGTACCGGCTGCGAGGCTCTTCCGTTACAGAGGGCAAC 2007
 QY 561 LeuAlaSerHisLysThrValHisThrGlyGlyLysProTyrArgCysAsnIleCysGly 580
 DB 2008 CTCGCGACGACCAACACGTCATACCGGTGAGAAACCTTATCTTGCAACATCTGTGGG 2067
 QY 581 AlaGlnPheAsnArgProAlaAsnLeuLysThrHisThrArgIleHisSerGlyGluLys 600
 DB 2068 GCCCAGTTCAACCGGCGAGCCCACTGAAACCCCACTCGAATTCATCTTGGAGAGAG 2127

QY 601 ProTyrLysCysGluThrCysGlyAlaArgPheValGlnValAlaHisLeuArgAlaHis 620
 DB 2128 CCTTACAAATGCAAACTCGCGAGCGACATTTGTACAGGTGGCCACCTCGGTCCAT 2187
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 QY 641 HisLeuGluThrLeuLysSerHisLeuArgIleHisThrGlyGlyLysProTyrHisCys 660
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 DB 2368 CATGGGCGCATCAACCAACCAAGTGAATACCGGCTGTCAAGCACTGACCTGCTCCG 2427
 QY 701 GluLeuProLysAlaCys 706
 DB 2428 GAGCTCCCAAGCCTGC 2445

RESULT 7
 PCT-US94-06669-1
 ; Sequence 1, Application PC/TUS9406669
 ; GENERAL INFORMATION:
 ; APPLICANT: Dallia-Favera, Riccardo
 ; APPLICANT: Chaganti, R.S.K.
 ; TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS
 ; TITLE OF INVENTION: bcl-6
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper & Dunham
 ; STREET: 30 Rockefeller Plaza
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: United States of America
 ; ZIP: 10112
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US94/06669
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/074,967
 ; FILING DATE: 09-JUN-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, John P.
 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 43771-A-PCT
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 977-9550
 ; TELEFAX: (212) 664-0525
 ; TELERX: 422523 COOP UI
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3720 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 328..2445
 ; PCT-US94-06669-1

Alignment Scores:

Prod. No.: 5,12e-277 Length: 3720
Score: 3763.00 Matches: 701
Percent Similarity: 99.4% Conservative: 1
Best Local Similarity: 99.3% Mismatches: 4
Query Match: 99.2% Indels: 0
DB: 6 Gaps: 0
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QY 21 AsnLeuAsnArgLeuArgSerArgAspIleLeuThrAspValValIleValIleSerArg 40
DB 388 AACCTTAATGCTCTCCGAGTCCAGACATCTTAAGTGTGTCAATGTTGTGAGCCGT 447
QY 41 GlnGlnPheArgAlaHisIleThrValIleuMetAlaCysSerGlyLeuPheTyrSerIle 60
DB 448 GAGCAGTTTAGAGCCCTTAATAACGTCCTCATGTGCTCGAGAGGCTGTTCTATACATC 507
QY 61 PheThrAspGlnLeuIleuIleuIleuSerValIleAsnLeuAspProGlnIleAsnPro 80
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QY 101 AsnIleMetAlaValMetAlaThrAlaMetTyrIleGlnIleuMetGlnHisValIleAspThr 120
DB 628 AACATCTGCTGTGATGCGCACCGGCTATGCTTACCTGCAATGAGCATGTTGTGAGACCT 687
QY 121 CysArgIlePheIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 140
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DB 748 GAAGAGTTCCTCAACAGCCGAGATGCTGATGCCCAAGACATGAGCTTACGAGGCTCT 807
QY 161 GlnValValIleGlnAsnLeuProLeuArgSerAlaProGlyCysGlnSerArgAlaPhe 180
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QY 221 AlaAsnProPheProIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 240
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QY 521 AsnGlnCysAspCysArgPheSerGlnGlnIleuIleuIleuIleuIleuIleuIleuIleu 540
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QY 541 HisSerAspIleuProIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 560
DB 1948 CACAGTGAACAACTTCAAGAGTGAAGCTGCCAGAGAGAGAGAGAGAGAGAGAGAG 2007
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DB 2008 CTGCGAG 2067
QY 581 AlaGlnPheAsnArgProAlaAsnLeuIleuIleuIleuIleuIleuIleuIleuIleu 600
DB 2068 GCCAGATTCAACCGGCAG 2127
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QY 661 GlnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 680
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RESULT 9

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US-09-063-035-1
; Sequence 1, Application US/09063035
; Patent No. 616091
; GENERAL INFORMATION:
; APPLICANT: PEUKERT, Karen; HARNEL, Frank; and EILERS,
; APPLICANT: Martin
; TITLE OF INVENTION: Myc-binding zinc finger proteins,
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; TITLE OF INVENTION: their preparation and their use
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kell & Weinkauff
; STREET: 1101 Connecticut Avenue
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.2 Mb storage
; COMPUTER: IBM AT-compatible, 80486 processor
; OPERATING SYSTEM: MS-DOS version 6.1
; SOFTWARE: WordPerfect version 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/063,035
; FILING DATE: 21-APR-1998
; CLASSIFICATION: 514
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2680 base pairs
; TYPE: Nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..159
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 160..2571
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2572..2680
; US-09-063-035-1
; Alignment Scores:
; Pred. No.: 4,266-37 Length: 2680
; Score: 614.50 Matches: 204
; Percent Similarity: 40.9% Conservative: 102
; Best Local Similarity: 27.3% Mismatches: 289
; Query Match: 16.2% Indels: 154
; Gaps: 25
; DB:
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Db 445 GCCACTTCTCCCAATGTGAGACATCATCATCATGAGGCGCTGCGATGCTCAAGTCACTTGGCT 504
QY 129 GluAlaGluMetValSerAlaIleLysProProArgGlnGlnPheLeuAsnSerArgMet 148
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D	b					-----	522
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		523	-----	GGGGAAATGCCGAG		537	
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O	y	185	TyrSer-----	GLyLeuSerThrPro-----	ProLaseTyTrSerMet	197	
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D	b	658	-----	GAGAGGGCGCGGTCAAGCCCAAGATGGCGCACG		693	
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D	b	775	GCTGCCGACGAAGCTGAGCCGCTTTGTCCAGAGCTCGAGCAAGAAATGAGAGTAGAG			834	
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D	b	952	GAGAACGAGAAATGAGAGTACGCGGCAACACTCGCGGACAGAGCTCGCTCCGAGGCC			1011	
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D	b	1012	CGGGGCCCTCGCTCAGGACCTACGGGCAACGGACCGACGAGTCMAAGGCTCTACGGCTCGCTC			1071	
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D	b	1072	ATCCAAMAGTGGAGG-----	ACTGTGGAGAGAGTTCAACCACACCGGGAGAC		1119	
O	y	391	aProGlyGIYProGluGlnAlaGluLeuGlyARgLeuSerProArgalaTYrThrala--			410	
D	b	1120	TTCAAGCGGACACATCCGCATCCACAGGGGGAGAGCCCTTCTCGTGGCGGAGATGGACG			1179	
O	y	411	----	ProProAlaCyGBInProPrometGluPro-----	GIuaMbnLeuArlLeuGlnSe	427	
D	b	1180	AAGGCTTTTCCGACCGGCGCGGTGCAAGGCCCAATGAMAAGACGACACCCCTTGAA			1239	
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D	b	1240	CCCTACGGCTGGAGAGATGCCGGAAGAGCTAC--	-----	GCTCATACAGCGTG	1287	
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Qy      500 -----gluIwecIygluThrGlnserGluTyrsEarpSerSerCy 513
Db      1452 TTCCAAGATGCGCCACTGGAGACCACGACAGCAAGACAGACAAAGTCCCACTG 1511
Qy      513 agIu-----As 515
Db      1512 CGACAGAAGATTCACACAGGTAAGGAACTGAAGCCCACTGAAGATTCACATCGCTGA 1571
Qy      515 nglYAlaPhePheCyvaenGIuCyvaBPcyvArGpHeSerGIuGIuAlaSerIeulYvAr 535
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RESULT 10
US-09-949-016-1780
; Sequence 1780, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FaastSeq for Windows Version 4.0

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      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1242 TACAGAACTCATCTGAA-----GAGAAACCTTAT 1271
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      336 LysSerAspCysGlnPProAmaSerProThrGlu1a1aCysSerSer1aAma1aCysIle 355
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1272 AAA-----TGCAGAGAAATGTGTAATGCTTT 1298
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      356 LeuGln1a1aSerGly-----SerProProl1a1aLys 365
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1299 AGTCAAGTTCATTAATTTTCAGTCCATCAGAGAGTCCACAGTGAAGAAAAACCATACAAA 1358
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      366 SerProThraPProLys1a1aCysAsnTProLys1a1aLysPheLeu1a1aSer 385
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1359 TGCAGAGAGTGTGTAGAGGCTTCGGTTGG-----AGT 1391
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      386 LeuAsnGlnAma1aLysPProGlyGlyProGluGln1a1aLysArgLeuSerPro 405
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1392 GTTAATCTC-----CGTCTTCACCAAG 1412
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      406 ArgAlaTyThr1a1aPPro1a1aCysGlnPProMetGluProGluAmaLeuAspLeu 425
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1413 AGGATCCACAGGGGT-----1427
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      426 GlnSerProThryLeuSer1a1aSerGlyGluAspSerThryLeuProGln1a1aSerArg 445
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1428 GAGAGAGCTTATTAATGTAGAGAAATGTGTAGAGGCTTCACT-----CAGGTCGACAT 1481
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      446 LeuAsnAsn1a1aAmaArgSerMetThyGlySerProArgSerSerSerGlu----- 463
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1482 TTT---CACATTCATCAGAGAGTCCACATCGAGAGAAACCTTAAAGTGTATGTGT 1538
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      464 -----SerHis---SerProLeuTyRMetHis-----471
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1539 GGTAAAGGCTTCAGCCCAATTCACATTAATATGATCGAGAGTCCACACAGAGAG 1598
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      472 ---ProProLysCysThraSerSerGlySerGlnSerProGlnHis1a1aGluMetCysLeu 490
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Db      1599 AAGCCATACAAAGTGTAGCGGTGGGAAAGGCTTTACCCGTATATACAGATCTGCATAT 1658
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      491 HisThr1a1aGlyProThraPhe1a1aGluGluMetGlyGluThraGlnSerGluTySerAsp 510
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      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      511 SerSerCysGluAmaGly-----516
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1698 AAGAGAGTGTAGAGGCTTCAGTCAAGCTTCAATCTTCAAGTCCATCAGATGTCCAC 1757
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      517 -----AlaPhePheCysAsnGluCysAspCysArgPheSerGluGlu1a1aSer 532
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1758 ACTGGAGAGAAACGATTCAGTGTGAAACGTGTGGAGAGGCTTCAGTCCCTCAAG 1817
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      533 LeuTyRArgHisThrLeuGlnThraHisSerAspLysProTyRLeuCysAspArgCysGln 552
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1818 CTTCAAAACCATCAGCCAGATCCACATCGAGAGAAACCAATATGATGTGTGTGTGT 1877
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      553 AlaSerPheArgTyRLeuGlyAsnLeu1a1aSerHisLysThraValHisThrGlyGluLys 572
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1878 AAGAGCTTCAGTATATGATTCATTAATCTTAACTACACCAAGTAATTCACATCGAGAGAAA 1937
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      573 ProTyRArgCysAsn1a1aCysGlyAlaGlnPheAsnArgProl1a1aSerLeuTyRHis 592
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

Db      1938 CCATATTAATGTAGAGATGTGGAAAGGCTTCAGTTGGAGATCAATCTTCATGCAAT 1997
Qy      593 ThrArgLeuHisSerGlyGluLysProTyRLeuCysGlnThraCysGlyAlaArgPheVal 612
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1998 CAAGAGTTCAGTCCAGAGAGAAACCTTAAATGTGACAGAGTGTATAGAGCTTCAGT 2057
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      613 GlnVal1a1aHis1a1aLeuArg1a1aVal1a1aLeu1a1aSerHisGlyGluLysProTyRProCys 632
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      2058 CAGGCAATGATTTTTCGGTATCATCAGAGAGTCCATCTCGAGAGAGCAATCAATGT 2117
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      633 GlnLeuCysGlyThraArgPheArgHisLeuGlnThraLeuLysSerHisLeuArgLeuHis 652
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      2118 GGTGTGTGTGTAGAGGCTTCAGTCCAGTCCCTGTCTTCAATCCATCAGAGAGTCCAC 2177
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      653 ThrGlyGluLysProTyRHisCysGlyLysCysAsnLeuHisPheArgHisLysSerGln 672
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      2178 ACCGGGAGAAAGCAATACAAATGTGTGTGTGTGAAAGGCTTGTATGATACAGTTCGAC 2237
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      673 LeuArgLeuHisLeuArgGlnLysHisGly 682
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      2238 TTTATATACATCAGAGAGCCACACTGGA 2267
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RESULT 13
US-09-620-312D-1084
; Sequence 1084, Application US/09620312D
; Patent No. 6569682
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Adundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aйдong J.
; APPLICANT: Wang, Jіan-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yundong
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghaet
; APPLICANT: Dimaіac, Radoje T.
; TITLE OF INVENTION: No. 6569682el Nucleic Acids and
; FILE REFERENCE: 784CIP28
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pc FL_genes Version 1.0
; SEQ ID NO 1084
; LENGTH: 2920
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (87)..(1922)
US-09-620-312D-1084

Alignment Scores:
Pred. No.: 2,61e-28 Length: 2920
Score: 500.00 Matches: 170
Percent Similarity: 34.9% Conservative: 81
Best Local Similarity: 23.6% Mismatches: 208
Query Match: 13.2% Indels: 260
DB: Caps: 23

US-10-755-889-18 (1-706) x US-09-620-312D-1084 (1-2920)

```

Oy	5	AlaHisSerCysIleGlnPheThrArgHisAlaIleSerAspValLeuLeuMetLeuAsnArg	24
Db	75	TCTGATATCAAAATGAGATTCGGACCACTGTGAGCACCTTTAGAGAGACTGAACA	134
Oy	25	LeuHisSerArgAspIleLeuThrAspValIleValIleValSerArgGluInPheArg	44
Db	135	CAGCGGGAAGACGGTTTTCTGTGTAGCTGTACATGATGTATGGGAATTCAGATTAA	194
Oy	45	AlaHisIleValThrValLeuMetAlaCysSerGlyLeuPheTyrSerIlePheThrAspGln	64
Db	195	GCTCATAGGAAGATGCTGGCCCTCTTACTGTAGTATTTGGTGGCGATCTACAGAAACACT	254
Oy	65	LeuIysCysAsnLeuSerValIleAsnLeuAsp---ProGluIleAsnProGluInIlyPhe	83
Db	255	TCTGAAACAAT-----GCTTTCTTATTCAGAGTCAGGTGAAGCTGTATGGATTT	305
Oy	84	CysIleLeuLeuAspPheMetTyrThrSerArgLeuAsnLeuArgGluInIlyAsnIleMet	103
Db	306	CAGAAACCTGTGGAGTTTATATACACAGAACTTTAACTTTGACGTTGGATGTATAA	365
Oy	104	AlaValMetAlaThrAlaMetTyrLeuGlnMetGluHisValIleAspThrCysArg---	122
Db	366	GAAATTCATCAGCGTCGTACTATCTCAAGAGTGAAGAGTGGTCACTAAATGCAAAATA	425
Oy	123	-----LysPheIleIlyValSerGluAlaGluMetValSerAlaIleIys	137
Db	426	AAGATGGAAGATTTGCTTTATTTGCTAACTCTTCTTACAGAGATTCCTAGATTACT	485
Oy	138	ProProArgGluGluPheLeuAsnSerArgMetLeuMetProGluAspIleMetAlaTyr	157
Db	486	GGAACCATTTGAA-----TTGAATCAACAGACTTGCTCT-----	518
Oy	158	ArgGlyArgGluValIleValGluAsnAsnLeuProLeuArgSerAlaProGlyCysGluSer	177
Db	519	-----CTTACTCTCGAGAT-----	533
Oy	178	ArgAlaPheAlaProSerLeuTyrSerGlyLeuSerThrProProAlaSerTyrSerMet	197
Db	533	-----	533
Oy	198	TyrSerHisLeuProValSerSerLeuPheSerAspGluInPheArgAspValArg	217
Db	534	-----TATATATATCGAGAAATCAGAAATGATTC	563
Oy	218	MetProValAlaAsnProPheProIysGluArgAlaLeuProCysAspSerAlaArgPro	237
Db	564	ACAGATTGATTCAGGCAAAATCCTTAACAAGCGCGTTA-----	602
Oy	238	ValProGlyGluTyrSerArgProThrLeuGluValSerProAsnValCysHisSerAsn	257
Db	602	-----	602
Oy	258	IleTyrSerProIysGluThrIleProGluGluAlaArgSerAspMetHisTyrSerVal	277
Db	602	-----	602
Oy	278	AlaGluGlyLeuIysProAlaIleProSerAlaArgAsnAlaProTyrPheProCysAsp	297
Db	603	-----GCCAAA	608
Oy	298	IysPalaSerIysGluInIysArgProSerSerGluAspGluIleAlaLeuHisPheGlu	317
Db	609	AAGTCATCTCAACGAAAGAAAGAGAAAGAGCT-----TTCAAC	647
Oy	318	ProProAsnAlaProLeuAsnAlaGlyIysGlyLeuValSerProGlnSerProGluIysSer	337
Db	648	TCGCCCAAAAACAGGCAAGATAA-----ACACTGCAATATCCC-----AGT	689
Oy	338	AspCysGluInProAsnSerProThrGluAlaCysSerSerIysAsnAlaCysIleLeuGln	357
Db	690	GACATCTTGAGAGATGCATCTGTGAATTATTCCTAGATCAAAAT-----	734

Oy	358	AlaSerCylSerProProAlaLysSerProThrLysAspProValaCysAenTrpLys	377
Db	735	-----AAAGTCCCAACA-----	746
Oy	378	TyrlValPheIleValLeuAenSerLeuAenGlnAvalLysProGlyGlyProGlnGln	397
Db	747	-----CCTGGTAGTA-----	755
Oy	398	AlaGluLeuClLysArgLeuSerProAlaGlyLysTrpAlaProProAlaCysGlnProPro	417
Db	756	GAACAAAGTTCACAAATATTAAT	776
Oy	418	MetGluProGluAenLeuAenPheGlnSerProThrLysLeuSerAlaSerGlyGluAsp	437
Db	777	-----GATATTTCCAAACTCGAG-----TTGACATCAAGTTTGCGAA	812
Oy	438	SerThrIleProGlnAlaSerArgLysLeuAenIleValAenArgSerMetThrGly--	456
Db	813	AATACTTTTCCAGACACAAGATATTTGTCACACCTGTTCCAGTGAAACCGAAACGTGGAAAA	872
Oy	457	---SerProArgSerSerSerGlnSerHisSerProLeuTrpMetHisProProLysCys	475
Db	873	TCACAGCCAACTGTGCTCGAAAGAAACCTCT--ATGCTCT	911
Oy	476	ThrSerCysGlySerGlnSerProGlnIleAlaGluMetCysLeuHisThrAlaGlyPro	495
Db	912	AATTAAGCCAGCGTCGAAGAGTCTTATAGAGCGGAG-----	947
Oy	496	ThrPheAlaGluGluMetGlyGlyThrGlnSerGlyTrpSerAspSerSerCysGluAen	515
Db	948	AACCTCCGGGAGAGCTCGATCCAGAGGTATTTCCAAAGCCAAAGCA-----	992
Oy	516	GlyAlaPhePheCysAenGluCysAspCysValArgPheSerGluGlnAlaSerLeuLysArg	535
Db	993	-----ATGTGTAACACATGTGGAAAGTGTTCAGAAAGCCACAGTTTGAGAAAG	1043
Oy	536	His-----	536
Db	1044	CACATGAGAAATACATAAAGAGTCAAACTTACGTCGACCTTATGTGGAAAGCATTT	1103
Oy	537	-----ThrLeuGlnThrHis-----SerAspLysProTrpLys	547
Db	1104	ACCCAAATGTAAACAGCTGAAACCCATGTAAAGATCATACAGGTGAGAAACCATACAA	1163
Oy	548	CysAspArgCysGlnAlaSerPheArgTrpLysGlyAenLeuAlaSerHisLysThrVal	567
Db	1164	TGTGAATTTGTGATAAAGATTTTGTCCAGAAAGTCAAGCTTCCATTAATGCGAATG	1223
Oy	568	HisThrGly--GlyLysProTrpArgCysAenIleCysGlyAlaGlnPheAenArgPro	586
Db	1224	CATCATGGTGAAGAAACCCCTATTAATGTATGATATGCAATTCACGTTTGCAACTTCT	1283
Oy	587	AlaAenLeuLysThrHisThrArgLLeHisSerGlyGlyLysProTrpLysCysGlyThr	606
Db	1284	AGCAATTCGAAAGTTCATGACAAAGGAGATGTGAGAGAAAGCCATATGTCTGTGATAG	1343
Oy	607	CysGlyAlaArgPheValGlnValAlaHisLeuArgAlaHisVal-----LeuIle	623
Db	1344	TGTGGACAGAAATTTTGTCTCAAGCCACACATGACCTTATGTCCTCGAAGGGCATTAAGT	1403
Oy	624	HisThrGlyGlyLysProTrpProCysGlyIleCysGlyLysThrArgPheArgHisLeuGln	643
Db	1404	-----GGAGAAAGCCTTATGTATGTGATACCTGTGTGGAAGGCAATTTGCTGTCTAGT	1457
Oy	644	ThrLeuLysSerHisLysLeuArgLLeHisThrGlyGlyLysProTrpHisCysGlyLysCys	663
Db	1458	TCTCTTATCACTCATTTCTCGAAACATACAGAGTGAATAAACATACATATGTGGTATTTGT	1511
Oy	664	AenLeuHisPheArgHisLysSerGlnLeuArgLeuHisLysLeuArgGlnLysHisGly	682
Db	1518	GGGAAAGATTTATTTCTCTCAGAGAGGTCAAAACACTTTCGGTCCCATACAGAG	1574

RESULT 14


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Db      1407 CATGTACCGGACGAGGAGGCTACGAGACGGTGTCTTACGGGGACAATTGTATGTGTGCAT 1466
Qy      476 rserCyglYserGlnSerProGln-----H18A1agLumetCyaleuH18th 492
          |||
Db      1467 TCCCTGCGGCAAGAGGCTTCCCGACGCTGTAGACAGCTCAATGGCGACGTGAGACTCACAC 1526
Qy      492 r1aag1yProthPha1aag1uGlumetGly-----G1uThr-----G1 505
          |||
Db      1527 GAGAGAAAGACTTATCATCAAGAGAGAGGGGCGCTACGAGACAGGACAGTGGGGTCCCA 1586
Qy      505 nserGluYrSerAserSerSerCygluAnGly1aPhePheCyAanGluCyAserCy 525
          |||
Db      1587 GAGAGAGCGCGACGACCTGTACGACCCCGAGTGGCGCTAC----- 1626
Qy      525 aArgPheSerGluGluAlaSerleuYarGht18th18uGlnThH18SerAryPr 545
          |||
Db      1627 -----ACGGCTGAGCCCGCGGC 1643
Qy      545 oYrYrYsCyAaPArCyseGlnAlaSerPheArGTYrYsGlyAanleuAlaSerH18y 565
          |||
Db      1644 CTTCAGGTGTCGCTGTCCGAGAAAGACTTCAAGACCCAGCCAGCTGGCGGACGACA 1703
Qy      565 rThrValH18thGly1uYrProTYrArGyCyAan11eCyseGly1aGlnPheAanr 585
          |||
Db      1704 GAAAGACGACGTGGCTGACACGGCGCTTCCCTCAACATCTGTGGCAAAATGTTCAAGCA 1763
Qy      585 gProAlaAnleuYrThH18thArGlnH18SerGlyGluYrProTYrYrYsG1 605
          |||
Db      1764 GCGCGGACCATGACCGGTACATGCGAGACCATGGCGCTGAACCCCTTCCCTGCA 1823
Qy      605 uThrCyG1yAlaArGpPheValGlnValAlaH18leuArGAlaH18Val1eulH18th 625
          |||
Db      1824 TGAGTGTGGATGGATGGCTTCCACCGCTCAAGTACCGGCTTCAAGACATGGTGTGACATC 1883
Qy      625 rGlyGluYrProTYrProCyseGlu1eCyseGly1uThArGpPheArGht18uGlnThr1e 645
          |||
Db      1884 GGGGAGAAACCTTACAGAGTGGCGAGCTGTGGGGGCAAGTTCAACCAGCAGCGCAACCT 1943
Qy      645 uYrSerH18leuArGlnH18thArGlyGlu-----YrPro----- 657
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Db      1944 CATCAGCCACCTGGCATGACACCTTCCCTCTGAAGACCAAAAGACCGCGGGCGGC 2003
Qy      658 -TYrH18CyseGluYrCyse 663
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Db      2004 CCACTATGCCAACCCTTGC 2022

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US-10-120-988-145
Alignment Scores:
Pred. No.: 3 448-28
Score: 498.50
Percent Similarity: 37.64
Best Local Similarity: 25.24
Query Match: 13.14
Gaps: 26

US-10-755-889-18 (1-706) x US-10-120-988-145 (1-2948)
Qy      9 11eGlnPheThArGht18A1aSerArPVal1euleuAnleuAanrYrYsG1eArG 28
          |||
Db      199 ATGAGAGTGGCCAGGACGACCTGCAAGAGACCTGCTGACAGCTTGAACAGAGGACCAAG 258
Qy      29 Aep11eulThArPVal1a11eVal1a18erArG1uGlnPheArGAlaH18thYrThr 48
          |||
Db      259 GCGTTCCTGTGTGAGTCAATCATGTGTGAGAACTCCATCTTCCGGGCGCACAAAGAAC 318
Qy      49 Val1eulMetAlaCyseArGly1eulPheYrSer11ePheThArPGL1eulYrCyAan 68
          |||
Db      319 GTCTAGCCGCGCAGC-----ACATCTATTTCAGTCCCTGCTGTGCAC 363
Qy      69 LeuSerVal11eAnleuArPProGlu---11eAnProGluGlyPheCy11eLeu 87
          |||
Db      364 GAAACCTCATCACTGTGACAGACATGTGTGACAGTCCACAGATGTTCCAGCAGATCTTG 423
Qy      88 AepPheMetYrThSerArGleu-----AanleuArG1uGlyAan11eMet 103
          |||
Db      424 GACTTCATCTTACACAGGCAAGCTGTGCCAGCAGCAGCCAGCCGAGCCCACTTCAAC 483
Qy      104 AlaVal1eulMetAlaThAr1aMetYr1eulGlnMetGluH18Val1a18PthrCyAryGly 123
          |||
Db      484 ACCCTCTACTGCGCGCAGTCACTTCAAGCTGCCGAGTGGAGCCCTGCGCGCC 543
Qy      124 Phe11eYr-----AlaSerGlu1aGluMetValSer1a1e 136
          |||
Db      544 AAATCAAGCAGACCGGCAAGCCCTTGGCTGTGGAGGGCGGGGTCCAGTGCATGGAG 603
Qy      137 YrProProArG1uGluPhe1eulAnSerArGht1eMet1eMetAla 156
          |||
Db      604 CGGCCCCCGGACGACGCGCTGTCCAGGCG-CTCTGTCAATCAAGCTCGATATCAAGG 662
Qy      157 TyrArGlyArGluVal1aGluAanleuPro----- 168
          |||
Db      663 GCTGTGTATGGGCGCAGGGGCGCCAGCGCCCGCAGAGCTCCCGCAAGCCAAAGGCTC 722
Qy      169 -----LeuArGSer1a1aProGly 174
          |||
Db      723 AGACCAATGAATCTTTCTTGTGTGTCTTACCAAGATAGCGTGAAGGTCTGGGCGGGC 782
Qy      175 CyseGluSerArGAlaPhe1a1aProSer1eulYrSerGly1eulSer-ThrProProAla 194
          |||
Db      783 TGT-----CTGCCAGCTGGCGGAGGCGGAGTCTGGGGGCTGCAGAG 827
Qy      194 rYrSerMetYrSerH18leuProValSerSer1eulPheSerArPGL1uGluPheAr 214
          |||
Db      828 CAGACCAACAGGAGAGCGGGGCTGCGAGCAGAGCTGGGCTTGGACTTGCACAGAA 887
Qy      214 GAePValArGmetProVal1a1aAnProPheProGly1uGluArGAla1eulProCyAaPse 234
          |||
Db      888 AAGCCACCTTGGCCCGTCCAGCCAGTCCC-----CACCTCACTCCGATAGCCG 941
Qy      234 r1aArGProValProGlyGluYrSerArGProThr1eulGlu1a1SerProAnValCy 254
          |||
Db      942 AGCCAGCTGAGGACAGCAACATGCTGCGCCCTGCGGCGCTGCTTCCCGCTTGC 1001
Qy      254 eH18SerAn11eYrSer-----ProYsGluThH18ProGluGlu1 269
          |||
Db      1002 CAACAGTGCCTTATTTAGCTGGGGGAGCCCTGATGAGCCATGATGTGAAGG 1061
Qy      269 aArgSerAepMetH18YrSerVal1a1aGluGly1eulYrProAla1aProSer1a1a 289

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Db      1062 GGGCGAGACACCTGAGCTGTGAG-----CGGCTGTGGGCA 1106
Qy      289 gaaanaLProTyrPheProCysAspLysAlaSerLysGluGluGluArgProSerSerG1 309
Db      1107 G-----CTTCGGAAGAGCTCCGGCACTCCACCTCGAAGAGAGTGGGGCAAGAGCA 1160
Qy      309 uaaepgLuIAlaLeuHisPheGluProProAsnAlaProLeuAsnArgLysGlyLeuVa 329
Db      1161 GCGTGTGGCTGGCTCCCTTTGAGCGGAGAGAGCA----- 1197
Qy      329 lserProGlnSerProGlnLysSerAspCysGlnProAsnSerProThrGluAlaCysSe 349
Db      1198 -GGGCGGAGAGGATCC-----TGC---CCGAGAGAGAGGAGGTGAGGGGCTGG 1241
Qy      349 rserLysAsnAlaCysAlaLeuGlnAlaSerGlySerProAlaLysSerProThra 369
Db      1242 GGACAGGGTTCCCAATGACATCTGCTAGTGG----- 1275
Qy      369 pProLysAlaCysAsnTrpLysLysTyrLysPheIleValLeuAsnSerLeuAsnGlnAs 389
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Db      1299 GGAGCCCCC-----TACCTCGCAAGAGAGAGAGAG- 1332
Qy      429 rLysLeuSerAlaSerGlyLysAspSerThrIleProGlnAlaSerArgLeuAsnAl 449
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Qy      449 eValAsnArgSerMetThrGlySerProArgSerSerSerGluSerHisSerProLeuTy 469
Db      1363 -----CAGAGCGGAGAGCGAGGGGCGAGCGGCATGCC--ACGCGCCACTA 1406
Qy      469 rMetHisProProLys-----CysEth 476
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Qy      476 rSerCysGlySerGlnSerProGln-----HisAlaGluMetCysLysHisEth 492
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Qy      492 rAlaGlyProThrPheAlaGluGluMetGly-----GluThr-----G1 505
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Qy      505 nSerGluTyrSerAspSerSerCysGluAsnGlyAlaPhePheCysAsnGluCysAspCy 525
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Qy      525 sarGpHeSerGluGluAlaSerLeuLysArgHisThrLeuGlnThrHisSerAspLysPr 545
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Qy      545 oTyrLysCysAspArgCysGlnAlaSerPheArgTyrLysGluAsnLeuAlaSerHisLy 565
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Qy      565 sThrValHisThrGlyLysLysProTyrArgCysAsnIleCysGlyAlaGlnPheAsnAr 585
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Qy      585 gProAlaAsnLeuLysThrHisThrArgIleHisSerGlyGluLysProTyrLysCysG1 605
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Db      1884 GGGCGAAGAACTTACAGAGTGCAGGTGGCGGGGCAAGTTACCCAGAGCGCAACTT 1943
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 Job time : 415 secs

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GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 2, 2006, 01:57:00 ; Search time 1444 Seconds
(without alignments)
4043.062 Million cell updates/sec

Title: US-10-755-889-18

Perfect score: 3793
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Scoring table: BLOSUM62
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Delop 6.0, Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the total score distribution.
and is derived by analysis of the total score distribution.

SUMMARIES

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2	3793	100.0	3536	7	US-10-776-827-90
3	3793	100.0	3536	7	US-10-755-889-17
4	3793	100.0	3536	7	US-10-755-889-65
5	3777	99.6	4506	6	US-10-252-157-169
6	3763	99.2	3720	3	US-09-107-058-1
7	3763	99.2	3720	3	US-09-761-117-1

8	1155	30.5	3676	6	US-10-295-027-15	Sequence 15, Appl
9	1155	30.5	3676	7	US-10-211-462-23	Sequence 23, Appl
10	1122.5	29.6	1749	3	US-09-815-379-3	Sequence 3, Appl
11	630	16.6	2741	9	US-10-974-440-92	Sequence 92, Appl
12	621.5	16.4	2769	5	US-10-037-270-309	Sequence 309, App
13	621.5	16.4	2769	6	US-10-117-722-309	Sequence 309, App
14	621.5	16.4	2769	9	US-10-122-851-309	Sequence 309, App
15	567	14.9	3451	9	US-10-486-977-45	Sequence 45, Appl
16	540	14.2	2289	9	US-10-477-646-22	Sequence 22, Appl
17	524.5	13.8	2826	7	US-10-221-625-117	Sequence 117, App
18	521	13.7	4950	5	US-10-034-934-13	Sequence 13, Appl
19	521	13.7	6190	7	US-10-676-2488-24	Sequence 24, Appl
20	514.5	13.6	2887	6	US-10-108-2604-859	Sequence 859, App
21	509.5	13.4	3349	8	US-10-108-2604-65	Sequence 65, Appl
22	508	13.4	2407	6	US-10-357-930-21308	Sequence 21308, A
23	508	13.4	2407	8	US-10-357-930-23642	Sequence 23642, A
24	508	13.4	2407	8	US-10-357-930-27150	Sequence 27150, A
25	508	13.4	2407	8	US-10-357-930-29533	Sequence 29533, A
26	504	13.3	2393	7	US-10-296-115-577	Sequence 577, App
27	503	13.3	3052	6	US-10-104-047-959	Sequence 959, App
28	501	13.2	2170	9	US-10-504-173-112	Sequence 112, App
29	501	13.2	2197	6	US-10-172-118-1228	Sequence 1228, App
30	501	13.2	2197	7	US-10-342-887-1228	Sequence 1228, App
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32	501	13.2	2197	9	US-10-756-149-169	Sequence 169, App
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37	498.5	13.1	2278	6	US-10-120-968-145	Sequence 145, App
38	498	13.1	3434	9	US-10-450-763-9676	Sequence 9676, App
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40	495.5	13.1	6793	8	US-10-723-860-1612	Sequence 1612, App
41	495.5	13.1	6994	8	US-10-723-860-16021	Sequence 6021, App
42	495	13.1	2320	6	US-10-305-720-1054	Sequence 1054, App
43	494.5	13.0	1947	6	US-10-136-728-57	Sequence 57, Appl
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ALIGNMENTS

RESULT 1
US-09-880-107-3271
Sequence 3271, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Scherf, Uwe
APPLICANT: Joseph G.
TITLE OF INVENTION: Gene Logic, Inc.
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 3271
LENGTH: 3536
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
OTHER INFORMATION: Genbank Accession No. US20020142981A1 U00115
US-09-880-107-3271

Alignment Scores:
Pred. No.: 0
Score: 3793.00
Percent Similarity: 100.0%
Length: 3536
Matches: 706
Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-755-889-18 (1-706) x US-09-880-107-3271 (1-3536)

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QY 61 PheThrAspGlnLeuLeuCyAsnLeuSerValIleAsnLeuAspProGluIleAsnPro 80
DB 508 TTTACAGACCAAGTTGAATGCCACTTAAGTGTATCATCTAATCTGAGATCAACCT 567
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QY 521 AsnGluCyAspCyAspArgPheSerGluGluAlaSerLeuLysArgHisThrLeuGlnThr 540
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DB 2248 CACCTTCAACCTGTAAAGGCACTCGCAATCCACACAGAGAGAAACCTTACATTTGT 2307
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RESULT 2

US-10-776-827-90
Sequence 90, Application US/10776827
Publication No. US20040132086A1
GENERAL INFORMATION:
APPLICANT: Horwitz, Kathryn
APPLICANT: Richer, Jennifer
TITLE OF INVENTION: Progesterone Receptor-Regulated Gene Expression and Methods Relat
TITLE OF INVENTION: Thierito
FILE REFERENCE: 2848-39
CURRENT APPLICATION NUMBER: US/10/776,827
CURRENT FILING DATE: 2004-02-10
PRIOR APPLICATION NUMBER: US/09/814,915
PRIOR FILING DATE: 2002-03-21
PRIOR APPLICATION NUMBER: 60/214,870
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PatentIn version 3.1
SEQ ID NO 90
LENGTH: 3536
TYPE: DNA
ORGANISM: Homo sapiens
US-10-776-827-90

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US-10-755-889-18 (1-706) x US-10-776-827-90 (1-3536)

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DB 1648 CCACAAAGCCAGCGGCTCAATTAACATGTGTAACAGGTCAAGAGGCTCTCCCGGAGC 1707
QY 461 SerSerGlySerHisSerProLeuTyrMetHisProProIySGlyThrSerCysGlySer 480
DB 1708 AGCAGAGAGGCACTACCACTCTTACATGACACCCCGAAGTGCAGTCTGCGGCTCT 1767
QY 481 GlnSerProGlnHisAlaGluMetCysLeuHisThrAlaGlyProThrPheAlaGluGlu 500
DB 1768 CAGTCCCAAGAGATGAGAGATGTGCTCCACACCGCTGCGCCCAAGTTCGTGAGAGAG 1827
QY 501 MetGlyGluThrGlnSerGlyIySGlyAspSerSerCysGluAnkGlyAlaPhePheCys 520
DB 1828 ATGGAGAGACCAAGTGTGATCTAGATTTCTAGCTGTAGAAAGCGGAGCTTCTTCTGC 1887
QY 521 AsnGluCysAspCysArgPheSerGlyGluAlaSerLeuIySGlyHisThrLeuGlnThr 540
DB 1888 AATGAGTGAATCTGCGCTTCTCTGAGAGAGGCTCACTCAAGAGGCACACGCTGCAAGC 1947

QY 541 H1S6SAsPlyserProTyrlsCySaAsPaCyGlnAlAsSerPheArgTyrlsGlyAen 560
DB 1948 CACAGTGAACCAACCTTCAAGTGTGACCGTGGCAGGCTCTTCCGCTCAACAGGCAAC 2007
QY 561 LeuAlAsSerHisPheThyValHisThrGlyGlyLysProTyrlsArgCySaAniLeCyGly 580
DB 2008 CTCGACAGCAACAAGACCGTCCATACCGGTGAGAAACCTTATGCTTGAACATCTGTGG 2067
QY 581 AlAGlnPheAsnAArgProAlaAsnLeuPheThrHisThrArgLLeHisSerGlyGlyLys 600
DB 2068 GCCCAATTCACACCGGCGAGCAACCTGAAACCCCACTGAATTCCTGAGAGAG 2127
QY 601 ProTyrlsCySaGlnThrCySaGlyAlaArgPheValGlnValAlaHisPheArgAlaHis 620
DB 2128 CCTTACAAATGCAAACTCGGAGGCAATTTGTACAGTGGCCCACTCCGTGCCAT 2187
QY 621 ValLeuLLeHisThrGlyGlyLysProTyrlsProCySaGlyLLeCySaGlyThyArgPheArg 640
DB 2188 GTGCTTATCCACACTGGTGAAGACCTTATCCTGTGAATCTGTGGACCCGTTCCGG 2247
QY 641 HisLeuGlnThrLeuLysSerHisPheArgLLeHisThrGlyGlyLysProTyrlsCySa 660
DB 2248 CACCTTCAGACTGTGAAGACCACTGGCATCCACAGAGAGAAACCTTACATTCAT 2307
QY 661 GluLysCySaAsnLeuHisPheArgHisPheSerGlnLeuArgLeuHisPheArgGlnLys 680
DB 2308 GAAAGTGTACCTGCTGCTTCCGTCAAAAGCAGCTGGAATTCATCTTGGCCCAAG 2367
QY 681 HisGlyAlaLLeThrAsnThyValGlnTyrlsArgValSerAlaThrAsnLeuProPro 700
DB 2368 CATTGGCCCATCAACAACCAAGTGCATACCGGTGCAGCCCACTGCTCCG 2427
QY 701 GluLeuProLysAlaCySa 706
DB 2428 GAGCTCCCAAGCTGTC 2445

RESULT 3

US-10-755-889-17
Sequence 17, Application US/10755889
Publication No. US20040171823A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
TITLE OF INVENTION: PATHWAY
FILE REFERENCE: D0284 NP
CURRENT APPLICATION NUMBER: US/10/755,889
PRIOR FILING DATE: 2004-01-13
PRIOR APPLICATION NUMBER: U.S. 60/440,068
PRIOR FILING DATE: 2003-01-14
PRIOR APPLICATION NUMBER: U.S. 60/469,757
PRIOR FILING DATE: 2003-05-12
NUMBER OF SEQ ID NOS: 823
SOFTWARE: PatentIn version 3.2
SEQ ID NO 17
LENGTH: 3536
TYPE: DNA
ORGANISM: Homo sapiens
US-10-755-889-17

Alignment Scores:

Pred. No.: 0 Length: 3536
Score: 3793.00 Matches: 706
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-10-755-889-18 (1-706) x US-10-755-889-17 (1-3536)

QY 1 MetaLAsSerProAlaAsPheSerCySILeGlnPheThrArgHisAlaSerAspValLeuLeu 20
DB 328 ATGGCTTCGCGGCTGACAGCTGATCCAGTTCAACCCGCAATGCACTGATGATTTCTTCTC 387

QY 21 AsnLeuAsnAArgLeuArgSerArgAspLLeuThrAspValValLeuValSerArg 40
DB 388 AACCTTAATCGTCTCGGAGTGCAGACATCTTGAATGTTGTATGTTGTAGCGGT 447
QY 41 GluGlnPheArgAlaHisPheThyValLeuMetAlaCySaSerGlyLeuPheTyrlsLe 60
DB 448 GAGCGATTAGAGCCCATAAACCGTCTCATGGGCTCCAGAGGCTGTTCATATGCAATC 507
QY 61 PheThrAspGlnLeuLysCySaAsnLeuSerValLLeAsnLeuAspProGlnLLeAsnPro 80
DB 508 TTACAGACCAATTAATGCAACTTATGTTGATCAATTCATGATCCAGATCAACCT 567
QY 81 GluGlyPheCySILeLeuLysAspPheMetTyrlsSerArgLeuAsnLeuArgGlyGly 100
DB 568 GAGGGAATCTGATCTCTCGGACTTCATGTACATCTCGGCTCAATTTGGGAGAGGC 627
QY 101 AsnLLeMetAlaValMetAlaThrAlaMetTyrlsLeuGlnMetGlnHisValValAspThr 120
DB 628 AACATCATGGCTGTATGGCCACCGCTATGTACCTGCAGATGAGACATGTTGTGACACT 687
QY 121 CySaArgLysPheLLeValAlaSerGlnAlaGlnMetValSerAlaLLeLysProProArg 140
DB 688 TTCGGAAGTATTATTAAGCCAGTGAAGCAGATGGTTTCTGCCATCAAGCTCTCGT 747
QY 141 GluGlnPheLeuAsnSerArgMetLeuMetProGlnAspLLeMetAlaTyrlsArgGlyArg 160
DB 748 GAAAGTTCCTCAACAGCGGATGCTGATGCCCAAGACATCATGCGGAGGTGCT 807
QY 161 GluValValGluAsnAsnLeuProLeuArgSerAlaProGlyCySaGlnSerArgAlaPhe 180
DB 808 GAGGTGTGGAACAACCTGCACTGAGAGACGCGCTGTGGTGTGAGAGCAACCTT 867
QY 181 AlaProSerLeuTyrlsSerGlyLeuSerThrProProAlaSerTyrlsSerHis 200
DB 868 GCCCCAGCTGTACAGTGGCTGTCCACACCGCCAGCTTATTCATGACAGCCAC 927
QY 201 LeuProValSerSerLeuLeuPheSerArgGlnGlnPheArgAspValArgMetProVal 220
DB 928 CTCCTGTGAGCAGCTCTCTTCCGATGAGAGTTCCGGAATGTCGAGTGCCTGG 987
QY 221 AlaAsnProPheProLysGlyLysArgAlaLeuProCySaAspSerAlaArgProValProGly 240
DB 988 GCCAACCCCTTCCCAAGAGGCGGCACTCCATGTGATGAGCCAGGCACTGCTGT 1047
QY 241 GluTyrlsSerArgProThrLeuGlnLysSerProAsnValCySaHisSerAsnLLeTyrlsSer 260
DB 1048 GAGTACAGCGGCGCACTTGAAGGTGCCCAATGTGTGCACAGCAATTCATTTCA 1107
QY 261 ProLysGlnThrLLeProGlnGlnLysArgSerAspMetHisTyrlsSerValAlaGlnGly 280
DB 1108 CCCAAGAAACAATCCCAAGAGGCAAGCAAGATGATACATACATGATGTGGCTGAGGCG 1167
QY 281 LeuLysProAlaAlaProSerAlaArgAsnAlaProTyrlsPheProCySaAspLysAspSer 300
DB 1168 CTCAAACCTGTCGCCCTCAGCGCCGAATGCCCTTACTTCCCTTGTGTACAGGCAAC 1227
QY 301 LysGlnGlnGlnArgProSerSerGlnAspGlnLLeAlaLeuHisPheGlnProProAsn 320
DB 1228 AAAAGAAAGAGAGACCTCTCGGAAGATGAGATGCCCTGATTTCCAGGCCCAAT 1287
QY 321 AlaProLeuAsnArgLysGlyLeuValSerProGlnSerProGlnLysSerAspCySaGln 340
DB 1288 GCAACCTTGAACCGGAAGGTCTGTATTCACAGAGCCCAAGAAATCTGATCTCCAG 1347
QY 341 ProAsnSerProThrGlnLysCySaSerLysAsnAlaCySILeGlnLysAspGly 360
DB 1348 CCCAATCCGCCCAAGAGGCTGCAAGTAAAGATGCTGATCTCCAGGCTTCTGCG 1407
QY 361 SerProProAlaLysSerProThrAspProLysAlaCySaAspThrLysTyrlsPhe 380
DB 1408 TCCCTTCACGCAAGGCCCACTGACCCCAAGCCTGCACTGGAAGAAATACAGATTC 1467
QY 381 LLeValLeuAsnSerLeuAsnGlnAsnAlaLysProGlnGlyProGlnGlnAlaGlnLeu 400

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1468 ATCTGCTCAACACCTTCAACCAAGACCAAGGAGGAGGCTGAGGAGGCTGAGCTG 1527
1468 ATCTGCTCAACACCTTCAACCAAGACCAAGGAGGAGGCTGAGGAGGCTGAGCTG 1527
401 G1YArgLeuSerProAlaArgAlaArgAlaProAlaCysGlnProPromeGluPro 420
1528 GGGCGGCTTTCCTCCCAAGGCTTACACGCGCCCACTGCTGCGAGCCACCACTGAGACCT 1587
421 G1UAsnLeuAspLeuGlnSerProThrLysLeuSerAlaSerGlyGluAspSerThrIle 440
1588 GAGAACTTTCAGCTCCAGTCCCAACCAAGTGTGAGTCCAGGAGGAGGAGTTCACCAATC 1647
441 ProGlnAlaSerArgLeuAsnAlaValAlaAsnArgSerMetThrLysSerProArgSer 460
1648 CCACAGCGAGCGCGGCTCAATACATGCTTACAGTTCATGAGCGGCTCTCCCGGAGC 1707
461 SerSerGlnSerHisSerProLeuThrMetHisProProLysCysThrSerCysGlySer 480
1708 AGCAGCGAGGAGGCTCAACCACTTACATGCAACCCCGAGAGTCCAGTCTGCGGCTCT 1767
481 GlnSerProGlnHisAlaGluMetCysLeuHisThrAlaGlyProThrPheAlaGluGlu 500
1768 CAGTCCCGCAGCAGTGCAGAGATGTGCTCCACACCGCTGCGCCAGCTTGCCTGAGAGAG 1827
501 MetGlyGluThrGlnSerGluThrSerAspSerSerCysGluAsnGlyAlaPhePheCys 520
1828 ATGGAGAGAGACCCAGTCTGAGTACTCAGATTCTAGCTGTGAGAACGGGCGCTTCTGTC 1887
521 AsnGluCysAspCysArgPheSerGluGluAlaSerLeuLysArgHisThrLeuGlnThr 540
1888 AATAGATGTACCTGCGCTTCTTGAAGAGGCTCTACCTCAAGAGGACCACTGCAAGACC 1947
541 HisSerAspLysProTyrLysCysAspArgCysGlnAlaSerPheArgTyrLysGlyAsn 560
1948 CACAGTGCACAACTCAAGTGTGACCGCTGCCAGGCTCTCCGCTCAACAGGCGAAC 2007
561 LeuAlaSerHisLysThrValHisThrGlyGluLysProTyrArgCysAsnAlaCysGly 580
2008 CTCCCGACGCCCAAGACCGTGCATACCGGTGAGAAACCTTATCGTTCGACATCTGAGGG 2067
581 AlaGlnPheAsnArgProAlaAsnLeuSerThrHisThrArgLysHisSerGlyGluLys 600
2068 GCCCAGTTCAACCGGCGCCGACCACTGAAACCCACACTCGAATTCACCTGAGAGAGAG 2127
601 ProTyrLysCysGluThrCysGlyAlaAlaArgPheValGlnValAlaHisLeuArgAlaHis 620
2128 CCTTACAAATCGAAACCTGCGAGGACGATTTTGTACAGGTGGGCCCACTCGGTCCAT 2187
621 ValLeuLysHisThrGlyGluLysProTyrProCysGluLysCysGlyThrArgPheArg 640
2188 GTGCTTATCCACACTGTGTGAGAGGCTTATCCTGTGAAATCTGTGGACCCGTTTCCGG 2247
641 HisLeuGlnThrLysSerHisLeuArgLysHisThrGlyGluLysProTyrHisCys 660
2248 CACCTTCAGACTCGAAGAGCCACTGCGAATCCACAGAGAGAAACCTTACCATTTGT 2307
661 G1UAspCysAsnLeuHisPheArgHisLysSerGlnLeuArgLeuHisLeuArgGlnLys 680
2308 GAGAAAGTTCATCTGCACTTTCGTGCAAAAGCCAGCGCTGCACTTTCGCGGAGAGAG 2367
681 HisGlyAlaIleThrAsnThrLysValGlnTyrArgValSerAlaThrAspLeuProPro 700
2368 CATGGCGGCATCACCAACCAAGGTGCAATACCGGTGTCAGCCACTGACCTGCTCG 2427
701 G1UeuProLysAlaCys 706
2428 GAGCTCCCAAGGCTGCTC 2445

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RESULT 4
US-10-755-889-65
; Sequence 65, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company

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; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
; TITLE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755, 889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440, 068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469, 757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 65
; LENGTH: 3536
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-755-889-65

Alignment Scores:
Pred. No.: 0 Length: 3536
Score: 3793.00 Matches: 706
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-10-755-889-18 (1-706) x US-10-755-889-65 (1-3536)

QY 1 MetAlaSerProAlaAspSerGlyGlnPheThrArgHisAlaSerAspValLeu 20
DB 328 ATGGCGCTCGCGGCTGACAGTGCATGATCCAGGAGGAGGAGTGTGAGCGGT 387

QY 21 AsnLeuAsnArgLeuAspSerArgAspIleLeuThrAspValIleValIleSerArg 40
DB 388 AACCTTATGCTCTCCGAGATCAGAGATCTTACATGATGTGATGTTGAGCGGT 447

QY 41 GlnGlnPheArgAlaHisLysThrValLeuMetAlaCysSerGlyLeuPheYSerIle 60
DB 448 GAGCAGTTTGAAGCCCATTAACCGTCTGATGCGCTGAGGAGGAGGAGTGTGAGCACT 507

QY 61 PheThrAspGlnLeuLysCysAsnLeuSerValIleAsnLeuAspProGluIleAsnPro 80
DB 508 TTTTACAGACCGGTTGAATGCAACCTTATGATGATCATGATCTGAGATCAACCT 567

QY 81 GlnGlyPheCysIleLeuLeuAspPheMetTyrThrSerArgLeuAsnLeuArgGluGly 100
DB 568 GAGGAGTTCGATCTCTCCGACTTCAATGATCACTCGGCTCAATTGCGGAGGAGG 627

QY 101 AsnIleMetAlaValMetAlaThrAlaMetTyrLeuGlnMetGluHisValValAspThr 120
DB 628 AACATCATGGCTGTGATGGCCAGCGCTATGATCTGAGATGAGCATGTTGTGACACT 687

QY 121 CysArgLysPheIleLysAlaSerGluAlaGluMetValSerAlaIleLysProProArg 140
DB 688 TGCCGGAAGTTTATTAAGCCAGTGAAGAGAGATGTTCTGCAACAGCTCTCGT 747

QY 141 GlnGlnPheLeuAsnSerArgMetLeuMetProGlnAspIleMetAlaIleArgGlyArg 160
DB 748 GAAAGATTCTCCACACCGGAGTGTGATGCTCCCAACATCATGAGGCTGAGTCTG 807

QY 161 GlnValValGluAsnLeuAspProLeuArgSerAlaProGlyCysGlnSerArgAlaPhe 180
DB 808 GAGGTGTGAGAAACCACTGCACTGAGAGGCGCCCTGAGTGTGAGAGAGAGGAGCTTT 867

QY 181 AlaProSerLeuTyrSerGlyLeuSerThrProProAlaSerTyrSerMetTyrSerHis 200
DB 868 GCCCGCAGCGGTACAGTGGCTGTCCACACCGCAGCGCTTATTCATGATCAAGCAC 927

QY 201 LeuProValSerSerLeuLeuPheSerAspGluGluPheArgValAlaGluMetProVal 220
DB 928 CTCCCTGTCAGACACTCTCTCTCTCCGATGAGAGATTTGCGAGTGTCCGATCCCTGTG 987

QY 221 AlaAsnProPheProLysGluArgAlaLeuProCysAspSerAlaArgProValProGly 240

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Db	988	GCCAACCCCTTCCCAAGAGCGGCACTCCCATGTGATAGTGGCAGGCCAGTCCCTGGT	1047
Qy	241	GIuYrSerArpProThrLeuGIuValSerProAnaValCysHisSerAanIlleYrSer	260
Db	1048	GAGTACAGACCGGCGCACTTGTGAAGGTGTCCCCCAATGTGTGCCACACAATATCTATTCA	1107
Qy	261	ProYrSGIuThrIleProGIuGIuValAArgSerApMethsYrYrSerValAlaGIuGIy	280
Db	1108	CCCAAGGAAACATCCCAAGAGGAGCAGAAGTATATGCACTACATGTGTGGCTGAGAGGC	1167
Qy	281	LeuYrSerProAlaAlaProSerAlaArgAanAlaProYrPheProCysAspLYrAlaSer	300
Db	1168	CTCAAACTGCTGGCCCCCTCAGGCCGAAATCCCCCTACTTCCCTTGTGACAGGCCAGC	1227
Qy	301	LYrSGIuGIuArgProSerSerSerGIuAspGIuIleAlaLeuHisApheGIuProAan	320
Db	1228	AAAGAGAAAGAGAGACCTCTCCGGAAGATGAGATTGCCCTGCATTTCCAGACCCCCCAAT	1287
Qy	321	AlaProLeuAanAlaGlyAsGIyLeuValSerProGIuInerProGIuLYrSerAspCYGIuIn	340
Db	1288	GCACCCCTCGAACCAGAGGGGTCTGGTTATGTCACAGAGCCCCCGAAATCTGACTGGCAG	1347
Qy	341	ProAanSerProThnGIuAlaCysSerSerYrAanAlaCysIleLeuGIuAlaSerGIy	360
Db	1348	CCCAACTGGCCACAGAGGCTTGACAGCATGTAAGATGCTGCATCTTCAGAGCTTGTGGC	1407
Qy	361	SerProProAlaLYrSerSerProThrAspProLYrAlaCysAanTrpLYrYrLYrAsPhe	380
Db	1408	TCCCTCCAGCCAGAGAGGCCCACTGACCCCAAGACCTGCAACTGGAAGAAATTAACAATTC	1467
Qy	381	IleValLeuAanSerLeuAanGIuAanAlaLYrProGIyGIyProGIuGIuAlaGIuLeu	400
Db	1468	ATCGTGCTCAACAGGCTTCAACAGAAATGCCAAACAGGGGGGCTGTGAGAGGCTGAACTG	1527
Qy	401	GIYrArgLeuSerProArGIAlaThYrThrAlaProProAlaCysGIuInProMethGIuPro	420
Db	1528	GGCGGCTTTCCCAAGAGCCCTACAGGCCCCCACTGTCTCCAGAGCAACCATGAAAGCT	1587
Qy	421	GIuAanLeuAspLeuGIuInSerProThrLYrLeuSerAlaSerGIyGIuAspSerThrIle	440
Db	1588	GAGAACTTGAACCTCCAGTCCCCCAACCAAGCTGAGTGCACAGGGAGAGACTCCACATTC	1647
Qy	441	ProGIuAlaSerArgLeuAanAanIleValAanArgSerMethThrGIySerProArSer	460
Db	1648	CCACAGGCGAGCCGGCTCAATTAACCTCTTAACAGGTCCACAGAGGGGCTCTCCCGCAGC	1707
Qy	461	SerSerGIuSerHisSerProLeuLYrMethHisProPOLySCTHrSerCysGIYSer	480
Db	1708	AGCAACGAGAGCACTCACTCACTCAATGACCCCCCGAAGTGCACCTCTGGGGCTCT	1767
Qy	481	GIuSerProGIuInHisAlaGIuMethCysLeuHisThrAlaGIYProThrPheAlaGIuGIu	500
Db	1768	CAGTCCCAACAGCATGACAGATGTGGCTCCACACCGCTGGCCCCAGCTTGGCTGAGAG	1827
Qy	501	MethGIyIuThrGIuInSerGIuLYrSerApSerSerCYrGIuAsnGIyAlaPhePheCys	520
Db	1828	ATGGAGAGAGACCACTGTAGTACTCAATTTCTAGCTGTGAGAACGGGGCTTCTTCTGC	1887
Qy	521	AasnGIyCYrAspCYrArgPheSerGIuGIuAlaSerLeuLYrBArGHisThrLeuGIuThr	540
Db	1888	AATGATGTATGATCGCGCTTCTCTGAGAGAGGCTTCACTCAAGAGGACACACGCTCAGAC	1947
Qy	541	HisSerAspLYrProYrLYrCysAspArgCYrGIuAlaSerPheArgTYrLYrGIYAan	560
Db	1948	CACAGTACAAACCTTACAAGTGTACCGGCTGCCAGGCTCTCTTCCGCTTACAAGGGCAAC	2007
Qy	561	LeuAlaSerHisLYrSerThrValHisThrGIyGIuLYrProYrArgCYrAanIlleCYrGIY	580
Db	2008	CTCGCCAGACCAACAAGCCGTCCATACCGGTGAGAAACCTTATCGTTGCAACATCTGTGGG	2067
Qy	581	AlaGIuInPheAanArgProAlaAanLeuLYrThrHisThrArgIleHisSerGIyGIuLYrS	600
Db	2068	GGCCAGTTTCAACCGGCGAGCCCAACTGAAACCCCACTGCATTCATCTCTGAGAGAAAG	2127

Oy		601	ProTylyscYsgIuthrCYsgIyalAargPheValGlnValahIsleuAgaLahIs	620
Dd		2128	CCCTACAAAGCGCGMAACTGGGAGCCCAAGATTGTATAGGTGGGCCACTTCGGCCCAT	2187
Oy		621	ValleuHlehIshThrgIygIulyrProTYrProcYsgIuleCYsgIyThrArgPheArg	640
Dd		2188	GTCCTTATCCACACTGTGTGAAGACCCTTAATCCCTGTGAATCTGTGGCACCCGTTCCGG	2247
Oy		641	HlsleugInthrleuLYSserHisleuArgIllehIshrgIyguLyProTYrhIsCys	660
Dd		2248	CACCTTGACACTGTGAAGAGCCACTCGAATCCACAAGAGAGAAACCTTACCATTTGT	2307
Oy		661	GIuLYrCYsbanleuHIsphethrghILyLSserGlnleuArgLeuHIsleuArgGlnLYs	680
Dd		2308	GAGAAGGTATACCTGCAGATTCCTGTCAAAAAGCCAGCTGGCACTTCACTTGGCCAGAG	2367
Oy		681	HlsGlyAlalIethrrAnthrLYsValGlntYrArgValSerAlathrAspleuProPro	700
Dd		2368	CATGGCCGCATCACCAACACCAAGTGTCAATACCGCTGTCAAGCACTGACCTGGCTCGG	2427
Oy		701	GIuLeuProLYsAlaCYs 706	
Dd		2428	GAGCTCCCCAAGCCTGC 2445	
 RESULT 5 US-10-252-157-169/c ; Sequence 169, Application US/10252157 ; Publication No. US20030190640A1 ; GENERAL INFORMATION: APPLICANT: Pearson, Mary TITLE OF INVENTION: GENES EXPRESSED IN PROSTATE CANCER FILE REFERENCE: PA-0027-1 US CURRENT APPLICATION NUMBER: US/10/252.157 CURRENT FILING DATE: 2002-10-01 PRIOR APPLICATION NUMBER: 60/295,048 PRIOR FILING DATE: 2001-05-31 NUMBER OF SEQ ID NOS: 501 SOFTWARE: PERL Program SEQ ID NO 169 LENGTH: 4506 TYPE: DNA ORGANISM: Homo sapiens FEATURE: NAME/KEY: misc.feature OTHER INFORMATION: Incyte ID No. US20030190640A1 977470.16c US-10-252-157-169				
 Alignment Scores:				
Pred. No.:	0	Length:	4506	
Score:	3777.00	Matches:	703	
Percent Similarity:	99.7%	Conservative:	1	
Best Local Similarity:	99.6%	Mismatches:	2	
Query Match:	99.6%	Indels:	0	
DB:	6	Gaps:	0	
 US-10-755-889-18 (1-706) x US-10-252-157-169 (1-4506)				
Oy		1	MetalaserProAlaAsperCYsllegInPheThrArgHIsaleuAspValleuLeu	20
Dd		3219	ATGGCTCGCGCGGTGACAGCTGTATCAAGTTCAACCCGCCACTGCGAGATGTTCTTCTC	3166
Oy		21	AseuLeuAenAglyeuarSerEArgAspiJeleuthrAspValvalIleValIaseArg	40
Dd		3159	AACCTTAATCGCTCCGAGATCGAGACATCTTGACTATATGTTCATTTGTGTGAGCCGT	3100
Oy		41	GIuGlnPhearGalAhIselyThrValIeuMetalaCYsSerGIyleuPhetySerile	60
Dd		3099	GAGCAGTTTAGGCCCATPAATAACGCTCTCATNGCCTCGACAGGCGCTGTTCTATAGCATC	3044
Oy		61	PheThrAspGlnleuLYrCYsbanleuSerValIleauLeuAspProGluIleasnPro	80

Db 3039 TTTACAGACCACTTGAATGCACTTAGTGATCATCTAGATCTCGATGCAACCT 2980
 Qy 81 Glu1GlyPheCys11IleuLeuAspPheMetYrThrSerArgLeuAenLysGly 100
 Db 2979 GAGGATTCCTGATCTCTCTGAGCTTCTGATGACATCTCGGCTCAATTTGGGAGAGGC 2920
 Qy 101 Asn11MetAlaValMetAlaThrAlaMetYrIleuGlnMetGlnIleValAspThr 120
 Db 2919 AACATCATGCTGTGATGGCCACCGCTATATGATCTGAGATGAGCATGTTGTGACACT 2860
 Qy 121 CysArgPhePhe11IleuAsaSerGluAlaGluMetValSerAlaIleLysProProArg 140
 Db 2859 TGCCGAAAGTTTATTAAGCCAGTGAAGACAGATGTTTCTGCAATCAAGCTCTCTGT 2800
 Qy 141 Glu1GluPheLeuAenSerArgMetLeuMetProGlnAsp11MetAlaYrArgGlyArg 160
 Db 2799 GAAGAGTTCTTCACAGCCGAGATGCTGATGCCCAAGACATCATGCTCATCGGGTCTGT 2740
 Qy 161 GluValValGluAenAenLeuProLeuArgSerAlaProGlyCyArgLysArgAlaPhe 180
 Db 2739 GAGGTGTGGAGAACACTTGCACCTGAGAGCGCCCTGGGTGTGAGAGACAGAGCTTT 2680
 Qy 181 AlaProSerLeuYrSerGlyLeuSerThrProProAlaSerYrSerMetYrSerHis 200
 Db 2679 GCGCCAGGCTGTACAGTGGCTGTCTCCACCGCAGCTCTTATTCATGATACAGCCAC 2620
 Qy 201 LeuProValSerSerLeuLeuPheSerAspGluGluPheArgAspValArgMetProVal 220
 Db 2619 CTCCCTGTACAGAGCTCTCTCTTCGATGAGAGTTTCGAGATGTCGGATGCTGTGTG 2560
 Qy 221 AlaAsnProPheProLysGluArgAlaLeuProCysAspSerAlaArgProValProGly 240
 Db 2559 GCCAACCCCTTCCCAAGAGACGGGCACTCCCATGTGATGTGACAGGCCAGTCCCTGT 2500
 Qy 241 GluYrSerArgProThrLeuGluValSerProAenValCysHisSerAsn11IleYrSer 260
 Db 2499 GAGTACAGCCCGGAGCTTGTGAGGTGTCCCAATGTGTCCACAGCAATATCTATTCA 2440
 Qy 261 ProLysGluThr11IleProGluGluAlaArgSerAspMetHisYrSerValAlaGluGly 280
 Db 2439 CCGAAGAAACATCTCCAGAAAGAGCAGAAATGATATGCACTACAGTGTGGCTGAGGGC 2380
 Qy 281 LeuYsProAlaAlaProSerAlaArgAsn11aProYrPheProCysAspLysAlaSer 300
 Db 2379 CTCAACCTGTGCTGCCCTCTCAGCCGGAATGCCCCCTACTTCCCTTGAGACAGGCCAGC 2320
 Qy 301 LysGluGluGluArgProSerSerGluAspGluIleAlaLeuHisPheGluProProAsn 320
 Db 2319 AAAGAAAGAGAGACCTCTCTCGGAAGATGAGATTTGCTGCAATTTGAGGCCCCCAT 2260
 Qy 321 AlaProLeuAenArgLysGlyLeuValSerProGlnSerProGlnLysSerAspCysGln 340
 Db 2259 GCACCCCTGAAACCGGAAGGCTGTGTATGCTCAGAGACCCCAAGAAATGACAGCCAG 2200
 Qy 341 ProAenSerProThrGluAlaCysSerSerLysAsnAlaCys11IleuGlnAlaSerGly 360
 Db 2199 CCGAATCTGGCCACAGAGTCTGAGCAGATGAATGCTGTGATCTTCAAGGCTTGTGGC 2140
 Qy 361 SerProProAlaLysSerProThrAspProLysAlaCysAsnTTPlyLysYrIlePhe 380
 Db 2139 TCCCTCCAGCCAGAGCCCACTGACCCCAAGGCTCTCACTGAGAAAGAAATACAGTTTC 2080
 Qy 381 IleValLeuAenSerLeuAenGlnAenAlaLysProGlyGlyProGluGlnAlaGluLeu 400
 Db 2079 ATCGTGCTCAAGAGCTCATCAATGCAATGCAACAGAGGGGCTGAGAGAGCTAGAGCTG 2020
 Qy 401 GlyArgLeuSerProArgAlaYrThrAlaProProAlaCysGlnProProMetGluPro 420
 Db 2019 GGCCTGCTTTCCTCCAGAGCTTACAGGGCCCACTGCTGCTGACAGCACTTGAAGCTT 1960
 Qy 421 GluAenLeuAspLeuGlnSerProThrLysLeuSerAlaSerGlyGluAspSerThrIle 440
 Db 1959 GAGAACTTGAACCTCAAGTCCCAACAGAGCTGAGTGCAGCGGAGAGATTCACCAATC 1900

Qy 441 ProGlnAlaSerArgLeuAenAen11ValAsnArgSerMetThrGlySerProArgSer 460
 Db 1899 CCAAGAGCCAGCCGGCTCAATTAATCATCTTAACAGTTCATGACGGGCTTCCCGCAGC 1840
 Qy 461 SerSerGluSerHisSerProLeuYrMetHisProProLysCysThrSerCysGlySer 480
 Db 1839 AGCAGGAGAGAGCCATCACATCTTCAATGACACCCCGAAGTGCAGTCTCGGCTCT 1780
 Qy 481 GlnSerProGlnHisAlaGluMetCysLeuHisThrAlaGlyProThrPheAlaGluGln 500
 Db 1779 CAGTCCCAAGCAGATGAGATGTCTTCCACACCGCTGCGCCCAAGTTCCTGAGAGAG 1720
 Qy 501 MetGlyGluThrGlnSerGluYrSerAspSerSerCysGluAenGluAlaPhePheCys 520
 Db 1719 ATGGAGAGAGCCAGTGTGATGATCAATGATCTTACTGATGAGAAAGGGGCTTCTTTC 1660
 Qy 521 AsnGluCysAspCysArgPheSerGluGluAlaSerLeuLysArgHisThrLeuGlnThr 540
 Db 1659 AATGAGTGTACGTGCGCTTCTGAGAGAGGCTCACTCAAGAGGCACAGCTGACAGAC 1600
 Qy 541 HisSerAspLysProYrLysCysAspArgCysGlnAlaSerPheArgYrLysGlyAsn 560
 Db 1599 CACAGTACAAACCTTACAAAGTGTGACCGCTGCAGGCTCTTCTGCTCAAGGGGCAAC 1540
 Qy 561 LeuAlaSerHisIleYrThrValHisThrGlyGluLysProYrArgCysAsn11IleCysGly 580
 Db 1539 CTGCGCAGCCACAGACCGTTCATACCGGTGAGAAACCTTATGCTTGCACATCTGTGGG 1480
 Qy 581 AlaGlnPheAenArgProAlaAenLeuYrThrHisThrArg11IleHisSerGlyGluLys 600
 Db 1479 GCCAGTTCACCGGCCAGCCAGCACTGAAAACCACTGAAATTCATCTGAGAGAGAG 1420
 Qy 601 ProYrLysCysGluThrYrGlyAlaArgPheValGlnValAlaHisIleuArgAlaHis 620
 Db 1419 CCTCAAAATGCGAAACCTCGGAGGACAGATTGTGATGAGTGGGCCCACTTCGGCCAT 1360
 Qy 621 ValLeuIleHisThrGlyGluLysProYrProCysGlu11IleCysGlyThrArgPheArg 640
 Db 1359 GTGCTTATTCACATGTGTGAGAAAGCTTATCTCTGTAAATCTGTGCAACCGGTTCCGG 1300
 Qy 641 HisLeuGlnThrLeuLysSerHisIleuArg11IleHisThrGlyGluLysProYrHisCys 660
 Db 1299 CACCTTCAAGCTGAAAGAGCCACTGCGAATTCACACAGAGAAACCTTACATTTGT 1240
 Qy 661 GluYsCysAenLeuHisPheArgHisLysSerGlnLeuArgLeuHisIleuArgGlnLys 680
 Db 1239 GAGAAGTGTACCTGATTTCCGTCAAAAAGCCAGCTGCGCATTTCACTTCCGCCAGAG 1180
 Qy 681 HisGlyAlaIleThrAsnThrLysValGlnTyrArgValSerAlaThrAspLeuProPro 700
 Db 1179 CATGGCCCATCAACCAACCAAGGTGCAATACGGCGTGTGACGACTGACCTGCTCCG 1120
 Qy 701 GluLeuProLysAlaCys 706
 Db 1119 GAGCTCCCAAGGCTGTG 1102

RESULT 6

US-09-107-058-1
 ; Sequence 1, Application US/09107058
 ; Patent No. US20010010922A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dalla-Favera, Riccardo
 ; APPLICANT: Niu, Hui-Feng
 ; TITLE OF INVENTION: CLONING AND USES OF THE GENETIC
 ; TITLE OF INVENTION: LOCUS bcl-6
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper & Dunham LLP
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: United States of America

ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,058
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/43771-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3720 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 328..2445
US-09-107-058-1

Alignment Scores:
Pred. No.: 0 Length: 3720
Score: 3763.00 Matches: 701
Percent Similarity: 99.4% Conservative: 1
Best Local Similarity: 99.3% Mismatches: 4
Query Match: 99.2% Indels: 0
Gaps: 0
DB: 3

US-10-755-889-18 (1-706) x US-09-107-058-1 (1-3720)
QY 1 MetAlaSerProAlaAspSerCysAlIeGlnPheThrArgHisAlaSerAspValLeuLeu 20
DB 328 ATGGCCCTCGCGCGGTGACAGCTGTATCCAGTTCACCCGCGCATGCCAGGAGATGTTCTTCTC 387
QY 21 AsnLeuAsnArgLeuArgSerArgAspIleLeuThrAspValIleValValSerArg 40
DB 388 AACCTTAATGCTCTCCGAGTCGAGACATCTGATGATGTCATGTTGTTGAGCGGT 447
QY 41 GluGlnPheArgAlaHisIleThrValLeuMetAlaCysSerGlyLeuPheTyrSerIle 60
DB 448 GAGCAGTTTAGAGCCCAATAAAGGTCCTCATGCGCTGAGAGCGCTGTTCTATAGCATC 507
QY 61 PheThrAspGlnLeuLysCysAsnLeuSerValIleAsnLeuAspProGluIleAsnPro 80
DB 508 TTTAACAACCGATTGAATGCAACCTTAGTGATCAATCTAGATCTCTGAGATCAACCTT 567
QY 81 GluGlyPheCysIleLeuLeuAspPheMetTyrThrSerArgLeuAsnLeuArgGluGly 100
DB 568 GAGGAGATTTCGATCCCTCTGACTTCATGATCACTCGGCTCAATTTGGGAGAGGCG 627
QY 101 AsnIleMetAlaValMetAlaThrAlaMetTyrLeuGlnMetGluHisValValAspThr 120
DB 628 AACATCATGGCTGTGATGCGCCACGCGCTATGTACTGAGATGAGCATGTTGTGACACT 687
QY 121 CysArgLysPheIleLysAlaSerGluAlaGluMetValSerAlaIleLysProProArg 140
DB 688 TGCCGGAAGTTTATTAGGCGCAGAGAGAGATGTTTCTGCAATCAAGCTCTCTCGT 747
QY 141 GluGlnPheLeuAsnSerArgMetLeuMetProGlnAspIleMetAlaIleArgGlyArg 160
DB 748 GAAGAGTTTCTCAACAGCCGAGTCTGATGCCCCAACAACATCAATGAGGCTTCCGGGCGT 807
QY 161 GluValValGluAsnAsnLeuProLeuArgSerAlaProGlyCysGluSerArgAlaPhe 180

DB 808 GAGTGTGAGAAACACTGCTGAGAGCGCCCTGGGTGTGAGAGCAGACCTTT 867
QY 181 AlaProSerLeuTyrSerGlyLeuSerThrProProAlaSerTyrSerMetTyrSerHis 200
DB 868 GCCCCAGCTTTTACAGTGGCTGTCCACACCGCAGCTTTTATTCATGACAGCCAC 927
QY 201 LeuProValSerSerIleLeuPheSerAspGluGlnPheArgAspValArgMetProVal 220
DB 928 CTCCCTGTGACGAGCTCTCTTCTCCGATGAGAGTTTCGGGATGTCGCGATGCTGG 987
QY 221 AlaAsnProPheProLysGluArgAlaLeuProCysAspSerAlaArgProValProGly 240
DB 988 GCCAACCCCTTCCCAAGAGAGGCGGACTCCCATGTGATGAGCCAGGCGCACTCTCTGT 1047
QY 241 GluTyrSerArgProThrIleGluGluValSerProAsnValCysHisSerAsnIleTyrSer 260
DB 1048 GAGTACAGCGGCGCACTTTGAGAGGTTCCTCCCAATGTGTGACACGACATCTATTC 1107
QY 261 ProLysGluThrIleProGluGluValaArgSerAspMetHisTyrSerValaGluGly 280
DB 1108 CCCAAGAAACAAATCCAGAAAGGCGAGAGTATGACATTAAGTGTGCTAGAGGC 1167
QY 281 LeuLysProAlaAlaProSerAlaArgAsnAlaProTyrPheProCysAspLysAlaSer 300
DB 1168 CTCAAACCTGCTGCCCCCTCAGCCCGAAATGCCCCCTTCTCTTGTGACAAAGCCAGC 1227
QY 301 LysGluGluGluArgProSerSerGluAspGluIleAlaLeuHisPheGluProProAsn 320
DB 1228 AAAGAGAAAGAGAGACCTCTCTCGAAGATGATGCTCTCAATTCAGAGCCCCCAAT 1287
QY 321 AlaProLeuAsnArgLysIleValSerProGlnSerProGlnLysSerAspCysGln 340
DB 1288 GCAACCCCTGAACCGAAGGCTGTGTTAGTCCACAGAGCCCCCAGAAATCTACCTGCGAG 1347
QY 341 ProAsnSerProThrGluAlaCysSerSerLysAsnAlaCysIleLeuGlnAlaSerGly 360
DB 1348 CCCAATCGCCACAGAGGCTGCGAGAGTAAATGCTGATCCTCCAGGCTTCTGCGC 1407
QY 361 SerProProAlaLysSerProThrAspProLysAlaCysAsnTyrLysTyrSerPhe 380
DB 1408 TCCCTCTCCAGCAAGGCCCCCACTGACCCCAAGCTGAGAGGAGAAATACAAATTC 1467
QY 381 IleValLeuAsnSerLeuAsnGlnAsnAlaLysProGlyGlyProGluGlnAlaGluLeu 400
DB 1468 ATCGTCTCAACAGCTTCAACGAATGCCAACAAGGGGCGCTGAGAGGCTGAGCTG 1527
QY 401 GlyArgLeuSerProArgAlaTyrThrAlaProProAlaCysGlnProProMetGluPro 420
DB 1528 GGCCTGCTTCCCAAGAGCTTACACGCGCCCACTGCTGCGACGACCCATGAGGCT 1587
QY 421 GluAsnLeuAspLeuGlnSerProThrLysLeuSerAlaSerGlyGluAspSerThrIle 440
DB 1588 GAGAACCTTGACCTTCAAGTCCCAACCAAGCTGAGTGCAGAGGAGGAGACTCCACATC 1647
QY 441 ProGlnAlaSerArgLeuAsnAsnIleValaAsnArgSerMetThrGlySerProArgSer 460
DB 1648 CCAACAAGCAGCGGCTCAATAACATCGTTAACAGTTCATAGCGGCTCTCCCGCAGC 1707
QY 461 SerSerGluSerHisSerProLeuTyrMetHisProProLysCysThrSerCysGlySer 480
DB 1708 AGCAGGAGAGCAGCTCAACATCAATCGTTAACAGTTCATAGCGGCTCTCCCGCAGC 1767
QY 481 GlnSerProGlnHisAlaGluMetCysLeuHisThrAlaGlyProThrPheAlaGluGlu 500
DB 1768 CATCTCCCAACAGATACAGATGAGTCCCAACCGCTGCGGCCCACTTCTGTGAGAG 1827
QY 501 MetGlyGluThrGlnSerGluTyrSerAspSerSerCysGluAsnGlyAlaPhePheCys 520
DB 1828 ATGGAGAGACCAAGTCTAGTACTCAATTTCTAGCTGTGAGAACGGGCGCTTCTTCTGC 1887
QY 521 AsnGluCysAspCysArgPheSerGluGluAlaSerLeuLysArgHisThrLeuGlnThr 540

Db 1888 AATGAGTGTGACTGCGCTTCTCTGAGAGGCTTCACTCAAGAGCAGCAGCTGCAACC 1947
 Qy 541 HisSerAspLysProTyrLysCysAspArgCysGlnAlaSerPheArgTyrLysGlyAsn 560
 Db 1948 CAGAGTACAACCTTCAAGTGTGACCGCTGCGAGGCTCTCCCTACCAAGGCGCAC 2007
 Qy 561 LeuAlaSerHisLysThrValHisThrGlyGlyLysProTyrArgCysAsnIleCysGly 580
 Db 2008 CTCCCGCAGCACAAGACCGCTTCAACCGGTGAGAAACCTTATCTTCCATCATCTGTGG 2067
 Qy 581 AlaglnPheAsnArgProAlaAsnLeuLysThrHisThrArgIleHisSerGlyGlyLys 600
 Db 2068 GCCCAGTTCAACCGGCGAGGCACTGAAAACCACTGCAATTCATCTCGAGAGAGAG 2127
 Qy 601 ProTyrLysCysGlnThrCysGlyAlaArgPheValGlnValAlaHisLysLeuArgAlaHis 620
 Db 2128 CCGTACAATGCGAAACCTGGGAGGACGATTTTACAGGTGGCGCCACCTCGGCCCAT 2187
 Qy 621 ValLeuIleHisThrGlyGlyLysProTyrProCysGlnIleCysGlyThrArgPheArg 640
 Db 2188 GTGCTTATCCACACTGTGTGAGAGCCCTATCTCTGTGAAATCTGTGACACCCGTTTCCG 2247
 Qy 641 HisLeuGlnThrLysLysSerHisLysLeuArgIleHisThrGlyGlyLysProTyrHisCys 660
 Db 2248 CACCTTCAAGCTGTGAAGAGCCACTGTGAATCCACAGAGAGAGAACTTACATTTGT 2307
 Qy 661 GluLysCysAsnLeuHisPheArgHisLysSerGlnLeuArgLysHisLysLeuArgGlnLys 680
 Db 2308 GAGAGGTATACCTGCACTTCCGTACAAAACCGAGCTGCACCTTCACTTGGCGAGAG 2367
 Qy 681 HisGlyAlaIleThrAsnThrLysValGlnTyrArgValSerAlaThrAspLeuProPro 700
 Db 2368 CATGGCGCATCAACAACAAGGTGCAATACCGGTGACGACACTGACCTGCTCCG 2427
 Qy 701 GluLeuProLysAlaCys 706
 Db 2428 GAGCTCCCAAGCCTGC 2445

RESULT 7

US-09-761-117-1
 Sequence 1, Application US/09761117
 Patent No. US20010012887A1

GENERAL INFORMATION:

APPLICANT: Daila-Favera, Riccardo
 Chaganti, Raju S.K.

TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS
 bcl-6

NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP
 STREET: 1185 Avenue of the Americas
 CITY: New York

STATE: New York
 COUNTRY: United States of America

ZIP: 10036
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/761,117

FILING DATE: 16-Jan-2001

CLASSIFICATION: <Unknown>
 ATTORNEY/AGENT INFORMATION:

NAME: White, John P.
 REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 0575/4371-A-PCT-US-Y
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 278-0400
 TELEFAX: (212) 391-0525

TELEFAX: 422523 COOP UI
 INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3720 base pairs
 TYPE: nucleic acid

STRANDEDNESS: double
 TOPOLOGY: linear

MOLECULE TYPE: cDNA
 FEATURE:

NAME/KEY: CDS
 LOCATION: 328..2445
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-761-117-1

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:
0	3763.00	3720	701
Percent Similarity:	99.4%	Conservative:	1
Best Local Similarity:	99.3%	Mismatches:	4
Query Match:	99.2%	Indels:	0
DB:	3	Gaps:	0

US-10-755-889-18 (1-706) x US-09-761-117-1 (1-3720)

Qy 1 MetAlaSerProAlaAspSerCysIleGlnPheThrArgHisAlaSerAspValLeuLeu 20
 Db 328 ATGGCTCGCGGCTGACAGCTGTATCCAGTTCAACCGGCATGCGAGGATGTTCTTCTC 387
 Qy 21 AsnLeuAsnArgLeuArgSerArgAspIleLeuThrAspValValIleValAlaSerArg 40
 Db 388 AACCTTATAGTCTCCGAGATCGAGACATCTTGACATGTTGTTCATTTGTGAGGCGGT 447
 Qy 41 GluGlnPheArgAlaHisLysThrValIleuMetAlaCysSerGlyLeuPheTyrSerIle 60
 Db 448 GAGCAGATTAGACCCCAATAAACGGTCTCATGAGCCCTGAGAGAGCGCTGTCTTAGCATC 507
 Qy 61 PheThrAspGlnLeuLysCysAsnLeuSerValIleAsnLeuAspProGlnIleAsnPro 80
 Db 508 TTTRACAGACCAAGTTGAAATGCAACCTTAGTGATGATCATATAGTCTGATCAACCT 567
 Qy 81 GluGlyPheCysIleLeuLeuAspPheMetTyrThrSerArgLeuAsnLeuArgGluGly 100
 Db 568 GAGGATTTGATCATCTCTGACCTTGCATGATACATCTGCGTCAATTTGCGGAGAGGC 627
 Qy 101 AsnIleMetAlaValMetAlaThrAlaMetTyrLeuGlnMetGlnHisValAlaAspThr 120
 Db 628 AACCTCATGCTGTGAGTGCACGCGCTATGACTGAGATGAGCAATGTTGTGACACT 687
 Qy 121 CysArgLysPheIleLysAlaSerGlnAlaGlnMetValSerAlaIleLysProProArg 140
 Db 688 TGCCGAAAGTTTATTAAGGCCAGTGAAGAGATGTTTCTGCCATCAAGCCTCTCGT 747
 Qy 141 GluGlnPheLeuAsnSerArgMetLeuMetProGlnAspIleMetAlaTyrArgGlyArg 160
 Db 748 GAAGAGTTTCTCAACAACCGGATGCTGATGCGCCCAAGACATGAGCTTACGGGCGT 807
 Qy 161 GluValValGlnAsnAsnLeuProLeuArgSerAlaProGlyCysGlnSerArgAlaPhe 180
 Db 808 GAGGTGTGTGAGAAACAACCTGCCACTGAGAGCGCCCTGTGTGTGAGAGAGGCTTT 867
 Qy 181 AlaProSerLeuTyrSerGlyLeuSerThrProProAlaSerTyrSerMetTyrSerHis 200
 Db 868 GCCCCAGCCGTGACAGTGGCTGTCCACACCGGCACTCTTATTTCCATGTACAGCCAC 927
 Qy 201 LeuProValSerSerLeuLeuPheSerAspGlnGlnPheArgAspValArgMetProVal 220
 Db 928 CTCCCTGTGACAGACCTCTCTTCTCGAGAGAGAGTTGGAGATGTCGGATCTCTGTG 987
 Qy 221 AlaAsnProPheProLysGlnArgAlaLeuProCysAspSerAlaArgProValProGly 240
 Db 988 GCCAACCCCTTCCCAAGAGGCGGCACTCCCATGATATGTGACAGCCAGTCCCTGTG 1047
 Qy 241 GluTyrSerArgProThrLeuGlnValSerProAsnValCysHisSerAsnIleTyrSer 260
 Db 1048 GAGTACAGCCGCGGCACTTGTGAGGTGTCCCAATGTGTGCCACAGCAATATCTATTCA 1107

Best Local Similarity: 38.3% Mismatches: 142
 Query Match: 30.5% Indels: 232
 Gaps: 15

US-10-755-889-18 (1-706) x US-10-295-027-15 (1-3676)

QY 1 MetLeuSerProAla-----AspSerCysIle-----GlnPheThrArgHis 14
 Db 141 ATGGGTTTCCCGCCGCGCCGAGAGAGCGTGGCTACCTCCGCGATTCTACCTCGCAC 200
 QY 15 AlaSerAspValIleuLeuAsnLeuAsnArgLeuArgSerArgAspIleLeuThrAspVal 34
 Db 201 TCTCCACAGCTGCTGGGCACTTCAAGAGCTGGCGCTCGCGGGAATCTCATCTGAGCTC 260
 QY 35 ValIleValIleSerArgIleuGlnPheArgIleHisIleArgIleValIleMetCysSer 54
 Db 261 ACGTGTGCTGGTGGCGGCAACCCCTCAGACACACAGAGAGAGTTCATCTCATCTGAGCT 320
 QY 55 GlyLeuPheThrSerIlePheThrAspGlnLeuIleCysAsnLeuSerValIleAsnLeu 74
 Db 321 GGCTTCTTCTATTCATATTTCCGGGCGCTGCGGAGTCCGGGAGTGGAGCTCTCTCTG 380
 QY 75 AspProGluIleAsnProGluIlePheCysIleLeuLeuAspPheMetThrSerArg 94
 Db 381 CCGCGGGGTCCTCCGAGCGAGGCTTCCCGCTTATGGACTTCACTTACACTTCGCGC 440
 QY 95 LeuAsnLeuArgIleGluIleAsnIleMetCysIleValIleMetCysLeuGlnMet 114
 Db 441 CTGGCGCTCTCTCCAGCCACAGCAGCAGCAGCTCTCAGCGCGCCACCTATTTCAGATG 500
 QY 115 GluHisValIleValAspThrCysArgIlePheIleValIleAspGlnIleGluMetValSer 134
 Db 501 GAGCAGCTGGTCCAGGCACTGCCACCGCTTCATCCAGGCGCAGC----- 542
 QY 135 AlaIleIleAspProArgGluGluIlePheLeuAsnSerArgMetLeuMetProGlnAspIle 154
 Db 542 ----- 542
 QY 155 MetAlaThrArgGlyArgGluValValGluAsnAsnLeuProLeuArgSerAlaProGly 174
 Db 542 ----- 542
 QY 175 CysGluSerArgAlaPheAlaProSerIleuThrSerGlyLeuSerThrProProAlaSer 194
 Db 542 ----- 542
 QY 542 ----- 542
 QY 195 TyrSerMetThrSerHisLeuProValSerSerIleuLeuPheSerAspGluIlePheArg 214
 Db 543 -----TATGAACTCTGGGCACTTC----- 563
 QY 215 AspValArgMetProValAlaAsnProPheProGlyArgAlaLeuProCysAspSer 234
 Db 563 ----- 563
 QY 235 AlaArgProValProGlyGluThrArgProThrIleuGluValSerProAsnValCys 254
 Db 563 ----- 563
 QY 255 HisSerAsnIleThrSerProGlyGluThrIleProGluGluAlaArgSerAspMetHis 274
 Db 563 ----- 563
 QY 275 TyrSerValAlaGluGlyLeuAspProAlaAlaProSerAlaArgAsnAlaProThrPhe 294
 Db 564 -----CTGGCGCCCTCG----- 575
 QY 295 ProCysAspIleAlaSerIleGluGluIleArgProSerSerGluAspGluIleAlaLeu 314
 Db 576 -----GAAGCAGAACCCCAACA----- 593
 QY 315 HisPheGluProProAsnAlaProLeuAsnArgIleGlyLeuValSerProGlnSerPro 334
 Db 594 -----CCCCAAGGCTCT-----CCACCAAGTATGATCC 623

QY 335 GlnIleSerAspCysGlnProAsnSerProThrGluAlaCysSerSerIleAsnAlaCys 354
 Db 624 AGGCGCTCCGAGAGACACCCAGACCCACTTACGATTCGAAAC----- 668
 QY 355 IleLeuGlnAlaSerGlySerProProAlaIleSerProThrAspProIleValaCysAsn 374
 Db 669 -----TGCACTGAAGGCCCTCCAGGCTCCAGGCTGACCCCAAGGCCCTGAC 719
 QY 375 TrpIleValIleThrPheIleValIleAsnSerIleuAsnGlnIleAlaIleProGlyGly 394
 Db 720 TGGAAAAAGTACAGTACATCTGCTAACTCT----- 752
 QY 395 ProGluGlnIleGluGlyArgLeuSerProArgAlaThrAlaProProAlaCys 414
 Db 753 -----CAGGCTCCCAAGCAGAGAGCTGTGGGAGAGAACTTGTGCTCACTTGGCC 809
 QY 415 GlnProMetGluProGluAsnLeuAspLeuGlnSerProThrIleuSerAlaSer 434
 Db 810 CAAAGCCAGGCTCCCAAGTGAAGAGAGCTCCAGCAGCAGCAGCAGCAGCAGCAGCAGC 869
 QY 435 GlyIleAspSerThrIlePro-----GlnAlaSerThrLeuAsnIleValAsnArgSer 453
 Db 870 AGTGAAGAAAGAACCACTTCTGCTCCAGAGCAGGCTC----- 908
 QY 454 MetThrGlySerProArgSerSerSerGluSerHisSerProLeuThrMetHisProPro 473
 Db 909 -----TCTCAACTGCTGCGCACTGTCAGTTC----- 935
 QY 474 LysCysThrSerCysGlySerGlnSerProGlnHisAlaGluMetCysLeuHisThrAla 493
 Db 936 -----AAATGTGG-----GCTCCAGCCAGTACCCCTTACCTCACAATCCAG 980
 QY 494 GlyProThrPheAlaGluIleGluMetGlyIleThrGlnSerGluThrSerAspSerCys 513
 Db 981 -----GCTCAAGACACTCTGATATCACTCTGAACCGGCTGCTCACTACCG 1028
 QY 514 GluAsnGlyAlaPhePheCysAsnGluCysAspCysArgPheSerGluGluAlaSerIleu 533
 Db 1029 GAAAGTAAATTTTCACTGCTCCAGACTGAGGCTGTGCGAGGCTCTATCCGGGCTG 1088
 QY 534 LysArgHisThrIleuGlnThrHisSerAspIleProThrIleCysAspArgCysGlnAla 553
 Db 1089 GAC-----TCTTGGTCTCTGGGAGAGAGACAAACCTTAAAGTCTCAGCTGCGGCT 1145
 QY 554 SerPheArgThrIleGlyAsnLeuAlaSerHisIleThrValHisThrGlyIleuAspPro 573
 Db 1146 TCGTTCGGCTACAAAGGCAACCTTGCAGTATCTGACAGTGCACAGGGGAAAGGCT 1205
 QY 574 TyrArgCysAsnIleCysGlyAlaGlnPheAsnArgProAlaAsnLeuIleThrHis 593
 Db 1206 TACCACCTGCTCAATCTCGGAGCCCGTATTAAACCGGACAGCAACCTGAAGAACCAACGC 1265
 QY 594 ArgIleHisSerGlyIleuAspProThrIleCysGlyAlaArgPheValGln 613
 Db 1266 CGATCTCAATCGGAGAGAGAGCCGTAATAGTGAAGCTGCGCTGCGCTTGTACAG 1325
 QY 614 ValAlaHisLeuArgAlaHisValIleuIleHisThrGlyIleuAspProThrCysGlu 633
 Db 1326 GTGGCACTCGGGGGGCGAGCTGTATCCACACCGGAGAGAGCCCTTACCTTGGCCCT 1385
 QY 634 IleCysGlyThrArgPheArgHisLeuGlnThrIleuIleSerHisIleuValIleHisThr 653
 Db 1386 ACGTGGAGAACCCCTTCCGCACTCGACCTTCAAGAGCCAGGCTTGGATCCACACC 1445
 QY 654 GlyGluIleAspProThrHisCysGlyIleCysAsnLeuHisPheArgHisIleSerGlnIleu 673
 Db 1446 GGAAGAGAGCTTACCTGAGCCCTGTGCTGATTTCCGGCAACAAGTCAACTG 1505
 QY 674 ArgLeuHisLeuArgGlnIleHisGlyAlaIleThrAsnThrIleValGlnThrArgVal 693
 Db 1506 CGGCTGATCTGGCCGAGAAACAGAGAGCTCTACCAACCAAGTGCATCCACACTT 1565

RESULT 9

US-10-211-462-23
Sequence 23, Application US/10211462
Publication No. US2004003495A1
GENERAL INFORMATION:
APPLICANT: Murray, Richard
APPLICANT: Glynn, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Atiz, Natascha
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and
FILE REFERENCE: 018501-006200US
CURRENT APPLICATION NUMBER: US/10/211,462
PRIORITY FILING DATE: 2003-02-13
PRIORITY APPLICATION NUMBER: US 03/784,356
PRIORITY FILING DATE: 2001-02-14
PRIORITY APPLICATION NUMBER: US 09/791,390
PRIORITY FILING DATE: 2001-02-22
PRIORITY APPLICATION NUMBER: US 60/310,025
PRIORITY FILING DATE: 2001-08-03
PRIORITY APPLICATION NUMBER: US 60/334,244
NUMBER OF SEQ ID NOS: 230
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 23
LENGTH: 3676
TYPE: DNA
ORGANISM: Homo sapiens
US-10-211-462-23

Alignment Scores:

Pred. No.: 2.55e-97 Length: 3676
Score: 1155.00 Matches: 268
Percent Similarity: 46.6% Conservative: 58
Best Local Similarity: 38.3% Mismatches: 142
Query Match: 30.5% Indels: 232
DB: 7 Gaps: 15

US-10-755-889-18 (1-706) x US-10-211-462-23 (1-3676)

QY 1 MetAlaSerProAla-----AspSerCysIle-----GlnPheThrArgHis 14
DB 141 ATGGGTTCCCGCCCGCCCGGAGGAGCGCTGGGCTACGTCGCGAGTTCACTCCGCGAC 200
QY 15 AlaSerApValIleuLeuAenLeuAenArgLeuArgSerArgApIleLeuThrAspVal 34
DB 201 TCCTCCGACGCTGGGCAACCTCAACGAGCTGGCGCGGAGATCTCACTGACGTC 260
QY 35 ValIleValIleSerArgGluGlnPheArgAlaHisIleThrValIleuMetAlaCysSer 54
DB 261 ACGCTGGTGGTGGCGGCAACCCCTCAGACACAAAGGCAAGTTCATCGCTGCAGT 320
QY 55 GlyLeuPheTyrSerIlePheThrAspGlnLeuLysCysAenLeuSerValIleAenLeu 74
DB 321 GGCCTTCTTCAATTATTTTCCGGGCGCGTCCGGAAGTCCGGGAGACGTCCTCTCTG 380
QY 75 AspProGluIleAenProGluGlyPheCysIleLeuLeuAspPheMetTyrThrSerArg 94
DB 381 CCGGCGGGGTCCGAAAGGAGAGGCTTCGCCCTCATATTTGACCTTCATGACATTCCGCG 440
QY 95 LeuAenLeuArgGluGlyAenIleMetAlaValMetAlaThrAlaMetTyrLeuGlnMet 114
DB 441 CTGGCGCTCTCTCCAGCACTGCAACGAGTCTTACGCGCGCCACCTATTTCAGATG 500
QY 115 GluHisValIleAspThrCysArgLysPheIleLysAlaSerGluAlaGluMetValSer 134
DB 501 GAGCAGCTGTCGCGGCGATGCCCGCTTCATCCAGGCCAC 542
QY 135 AlaIleLysProArgArgGluGluPheLeuAenSerArgMetLeuMetProGlnAspIle 154
DB 542 ----- 542

QY 155 MetAlaTyrArgGlyArgGluValValGluAenAenLeuProLeuArgSerAlaProGly 174
DB 542 ----- 542
QY 175 CysGluSerArgAlaPheAlaProSerLeuTyrSerGlyLeuSerThrProProAlaSer 194
DB 542 ----- 542
QY 195 TyrSerMetTyrSerHisLeuProValSerSerLeuAenPheSerAspGluGluPheArg 214
DB 543 -----TATGAACCTCTGGGCACTCC----- 563
QY 215 AspValArgMetProValAlaAenProPheProLysGluArgAlaLeuProCysAspSer 234
DB 563 ----- 563
QY 235 AlaArgProValProGluGlyTyrSerArgProThrLeuGluValSerProAenValCys 254
DB 563 ----- 563
QY 255 HisSerAenIleTyrSerProLysGluThrIleProGluGluAlaArgSerAspMetHis 274
DB 563 ----- 563
QY 275 TyrSerValAlaGluGlyLeuLysProAlaAlaProSerAlaArgAenAlaProTyrPhe 294
DB 564 -----CTGGCGCCCTCG----- 575
QY 295 ProCysAspLysAlaSerLysGluGluArgProSerSerGluAspGluIleAlaLeu 314
DB 576 -----GAAGCAGAACCCCAACA----- 593
QY 315 HisPheGluProProAenAlaProLeuAenArgLysGlyLeuValSerProGlnSerPro 334
DB 594 -----CCCCAAGCGCCCT-----CCACCAGTATGCTCC 623
QY 335 GlnLysSerAspCysGlnProAenSerProThrGluAlaCysSerSerLysAenAlaCys 354
DB 624 AGCGCTCCGAAGACACCCACCACTCATGATCTGAAAGC----- 668
QY 355 IleLeuGlnAlaSerGlySerProProAlaLysSerProThrAspProLysAlaCysAen 374
DB 669 -----TGCAAGTCAAGCCCCCGCCAGCTCAGCAGCCGACCCCAAGGCTTGCAAC 719
QY 375 TrpLysLysTyrLysPheIleValLeuAenSerLeuAenGlnAenAlaLysProGlyGly 394
DB 720 TGGAAATAATGACAGTACATCGTCTAAACTCT----- 752
QY 395 ProGluGlnAlaGluLeuGlyArgLeuSerProArgAlaTyrThrAlaProProAlaCys 414
DB 753 ---CAGGCTCCCAACAGGAGGAGCTGTCGGGAGAGAAGTTCTGCTCACTTCCGCC 809
QY 415 GlnProMetGluProGluAenLeuAenAspLeuGlnSerProThrLysLeuSerAlaSer 434
DB 810 CAAGCCAGGCTCCCAAGAGAGAGGCTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 869
QY 435 GlyGluAspSerThrIlePro---GlnAlaSerArgLeuAenIleValAenAspSer 453
DB 870 AGTGAAGAAGAACCCCTTCTGCTCCCAAGAGAGGCTC----- 908
QY 454 MetThrGlySerProArgSerSerGluSerHisSerProLeuTyrMetHisProPro 473
DB 909 -----TCTCAACTGCTGCACTGCACTG----- 935
QY 474 LysCysThrSerCysGlySerGlnSerProGlnIleAlaGluMetCysLeuHisThrAla 493
DB 936 -----AAATGTGG-----GCTCCAGCAGATACCCCTTCACTCATATCCAG 980
QY 494 GlyProThrPheAlaGluGluMetGlyGluThrGlnSerGlyTyrSerLysSerSerCys 513
DB 981 -----GCTAAGACACCTTGATGATCACTCTGAACGGGCTGTCATCCATCCAG 1028
QY 514 GluAenGlyAlaPhePheCysAenGluCysAspCysArgPheSerGluGluAlaSerLeu 533

[illegible]

```

GENERAL INFORMATION:
APPLICANT: HILLMAN, Jennifer L.
APPLICANT: BANDMAN, Olga
APPLICANT: LAL, Preeti
APPLICANT: YUE, Henry
APPLICANT: REDDY, Roopa
APPLICANT: TANG, Y. Tom
APPLICANT: GERSTIN, Edward H.
APPLICANT: ARVIZU, Chandra
APPLICANT: BAUGHN, Mariah R.
APPLICANT: AZIMZAI, Yalda
APPLICANT: LU, Dyrung Aina M.
TITLE OF INVENTION: Human Transcriptional Regulator Molecules
FILE REFERENCE: PF-0509 USN
CURRENT APPLICATION NUMBER: US/10/974,440
CURRENT FILING DATE: 2004-10-26
PRIOR APPLICATION NUMBER: US/09/674,743
PRIOR FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: PCT/US99/09935
PRIOR FILING DATE: 1999-05-04
PRIOR APPLICATION NUMBER: 60/084,254
PRIOR FILING DATE: 1998-05-04
PRIOR APPLICATION NUMBER: 60/095,827
PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: 60/102,745
PRIOR FILING DATE: 1998-10-02
NUMBER OF SEQ ID NOS: 130
SOFTWARE: PERL Program
SEQ ID NO 92
LENGTH: 2741
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID NO: 1484257CBI
US-10-974-440-92

Alignment Scores:
Pred. No.: 2,73e-48 Length: 2741
Score: 630.00 Matches: 208
Percent Similarity: 41.7% Conservative: 104
Best Local Similarity: 27.8% Mismatches: 290
Query Match: 16.6% Indels: 147
DB: 9 Gaps: 26
US-10-755-889-18 (1-706) x US-10-974-440-92 (1-2741)
QY 9 ILEGLPHEThrArgHisAlaSerAspValLeuLeuAsnLeuAsnArgLeuAsnArgSerArg 28
DB 201 ATGAGACTTTCCCAAGACACGACCGACGATCTTGGAAACGCTGAACACGACCGGACGCTG 260
QY 29 ASPLEuLeuThrAspValValValValValSerArgLeuArgLeuPheArgAlaHisIleValThr 48
DB 261 GGGCTTCTCTGAGATGACGACCTTGTGTGTGACGGGTGCTTCAAGCTTAAGCTCAATAAGCA 320
QY 49 ValLeuMetAlaCysSerGlyLeuPheTyrSerIlePheThrAspGlnLeuLysCysAsn 68
DB 321 GTCTTGCGCGCGCTGCAGCGACGATCTCAAGATGCTCTTCTGTGACGAG----- 368
QY 69 LeuSerValIleAsnLeuAspProGluIleAsnProGluGlyPheCysIleLeuLeuAsp 88
DB 369 AAGAGCGTGTGACTGACATCACTGCT--AAAGCGGACGAGCTCGGGGACGATGCTGGAG 425
QY 89 PHeMeTyTrThrSerArgLeuAsnLeuArgGluGlyAsnIleMetAlaValMetAlaThr 108
DB 426 TTTATGTACACGGCCAGACGCTGAGCCCTGAGAACGATGATGATGTGCTGGCGGTG 485
QY 109 AlMeCyTrIleuGlnMetClnHisValValAspThrCysArgLysPheIleLysAlaSer 128
DB 486 GCCACTTTCCTCAATGACGACATCACTCAACGCGCTGCCAT----- 527
QY 129 GIAlAGlMeTValSerIleIleLysProProArgGluGluPheLeuAsnSerArgMet 148

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Db 1660 CGGGCCCTCAAGTCCGAGAGTGTGGAGACATTCAACACTCAGGAGACTGAAAGC 1719
 Qy 535 GHIETHrLEuGINThrHisSer---AspLySProTYrLYSCysAspArgCysGINalase 554
 Db 1720 GCAC---CTTCGGATGCCAGCGGGAGAGAGCCCTTACGTGTGCATCCACTGCCAGCGACA 1776
 Qy 554 rPhEARgTYrLYrEGLYAsnLEuAlaSerHisLYrThVaHisrPhrGLYrLYrProTY 574
 Db 1777 GTTTCGACAGCCCGCGCTGTCCAGCGCGGACGTCCGACATTCACAGGTGTGAAGCCATG 1836
 Qy 574 rArgCYsAsnLEuCYsGLYAlaGINPhEAsnArgProAlaAsnLEuLYSThrHisThrAr 594
 Db 1837 CCAETGTGTGATGTGCGGTAAAGGCTTCAACCAAGCCAGCTCCCTCATCGCCCACTGCG 1896
 Qy 594 gILHisSerGLYrLYrProTYrLYrCysGLYrThrCysGLYAlaArgPhEValGINa 614
 Db 1897 CCAGACACCGGGAGAGAGCCCTTACGTGTGCGAGCGCTGCGAAGAGATTCGTCCAGTTC 1956
 Qy 614 lAlaHisLEuArgAlaHisValLEuHisLEuThrGLYrLYrProTYrProCYsGLY 634
 Db 1957 CAGCGAGTGGCCCATCATTCATTCGCCACACGACCAACATCCGCCACCAAGTGCAGCGT 2016
 Qy 634 eCYsGLYrThrArgPhEARgHisLEuGINThrLEuLYSerHisLEuArgGLIETHrGL 654
 Db 2017 GTGCAGCAGGCTTCGTGAAAGTGGGAGACTGTCCAGACCATCATTCATTCACACTGCG 2076
 Qy 654 YGLYrProTYrHisCysGLYrCysAsnLEuHisPhEARgHisLYrSerGINLEuAr 674
 Db 2077 AGAGAGGCTTACCTGTGATGATGAGTGTGGGCTTCAACCGGGTGAACAACCTGCG 2136
 Qy 674 gLEuHisLEuArgGLYrSHrGLYAlaILEThrAsnThrLYrValGINTYrArgValSe 694
 Db 2137 CTCCACGCTGACCGGTGCACAGGCGCAAGGCGACATCAAGATC----- 2182
 Qy 694 rAlaThrAspLEuProProGIN 701
 Db 2183 -----CTGAGAGCCCGAG 2194

RESULT 13

US-10-117-722-309

Sequence 309, Application US/10117722

Publication No. US20030219744A1

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom

APPLICANT: Liu, Chenghua

APPLICANT: Asundi, Vinod

APPLICANT: Zhang, Jie

APPLICANT: Dimaec, Radoje T.

TITLE OF INVENTION: No. US20030219744A1 Nucleic Acids and

FILE REFERENCE: Polypeptides

CURRENT APPLICATION NUMBER: US/10/117,722

CURRENT FILING DATE: 2002-04-04

PRIOR APPLICATION NUMBER: 09/620,312

PRIOR FILING DATE: 2000-07-19

PRIOR APPLICATION NUMBER: 09/552,317

PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: 09/488,725

PRIOR FILING DATE: 2000-01-21

NUMBER OF SEQ ID NOS: 1104

SOFTWARE: pc_fl_genes Version 1.0

SEQ ID NO 309

LENGTH: 2769

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (248) ..(2659)

US-10-117-722-309.

Alignment Scores:

Pred. No.: 1.74e-47

Score: 621.50

Length: 2769

Matches: 205

Percent Similarity: 41.0%
 Best Local Similarity: 27.4%
 Query Match: 16.4%
 DB: 6
 US-10-755-889-18 (1-706) x US-10-117-722-309 (1-2769)

Qy 9 lLEuGINPhrThrArgHisAlaSerAspValLEuAsnLEuAsnArgLEuArgSerArg 28
 Db 248 ATGACACTTCCCGACGACGACGACATGTCTTGAAACAGCTGAACGACGCGACACTG 307
 Qy 29 AspILEuThrArgAspValAlaValSerArgGLYrLYrPhEARgAlaHisLYrThr 48
 Db 308 GCGCTTCTGTGATCATCTGACCTTGTGTGTGAGCGGTTCACCTTAAGGCTCATAAAGCA 367
 Qy 49 ValLEuMetAlaCysSerGLYrLYrPhEARgTYrSerILEThrAsnArgGLYrLYrCysAsn 68
 Db 368 GTGCTGGCGGCTGACGAGTACTTCAGATGTCTTGTGTGACCG----- 415
 Qy 69 LeuSerValILEuAsnLEuAspProGINILEuAspProGINLYrPhEArgSILEuLEuAsp 88
 Db 416 AAGGACGTGTGACCTGACATCATG---AAGCGGACGCGCTGGGCGACGCTGAG 472
 Qy 89 PheMetTYrThrSerArgLEuAsnLEuArgGLYrLYrMetAlaValMetAlaThr 108
 Db 473 TTATGTACAGCGCAAGCTGAGCTGAGCTGAGACCTGAGAACGTGATGTCTGCGCGTG 532
 Qy 109 AlaMetTYrLEuGINMetGLYrHisValAlaAspThrCYsArgLYrPheILEuAlaSer 128
 Db 533 GCCACTTCTCCAAATGACGAGACATCATCGGCGCTGCATGCTCAAGTCACTTGCCT 592
 Qy 129 GLYrAlaGLYrMetValSerAlaILEuArgProProArgGLYrLYrPheLEuAsnSerArgMet 148
 Db 593 GAG-----CCGCTACCGAGCTT----- 610
 Qy 149 LeuMetProGINAspILEuMetAlaTYrArgGLYrValGINValGINAsnLEuPro 168
 Db 611 -----GGGCGAAATGCCGAG 625
 Qy 169 LeuArgSerAlaProGLYrCysGLYrSerArgAla-----PheAlaProSerLEu 184
 Db 626 GCGTTGGCGACAGAGAGGAGGACAGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 685
 Qy 185 TySer-----GlyLeuSerThrPro-----ProAlaSerTYrSerMet 197
 Db 686 CTGAGCAGGCTGAGCAGGAGGAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 733
 Qy 198 TySerHisLEuProValSerSerLEuLeuPheSerAspGLYrLYrPheArgValArg 217
 Db 734 -----AGGAGCTCAG 745
 Qy 218 MetProValAlaAsnProPheProLYrGLYrAlaLEuProCYsAspSerAlaArgPro 237
 Db 746 -----GAGAGGCGCGCGGTGAGGCCAGAGTGCGGCGCAGC 781
 Qy 238 ValProGLYrLYrTYrSerArgProThrLEuGLYrValSerProAsnValCYsHisSerAsn 257
 Db 782 GGTCCAGACAGACAGAGAGAGCCGAT----- 808
 Qy 258 lLEuTYrSerProLYrGLYrThrLEuProGLYrLYrAlaArgSerAspMetHisTYrSerVal 277
 Db 809 -----GCGCCCGGAGCGCGCGCTGTGAGCTCAAGCCAGACCCACAGAGTGCATG 862
 Qy 278 AlaGLYrLYrLEuLYrProAlaAlaProSerAlaArgAsnAlaProTYrPhEProCYsAsp 297
 Db 863 GCTGCGGAGAGAGCTGAGCGCGCTTGTTCGAGAGCTCGAGCAAGAAATGAGAGTGGAG 922
 Qy 298 LysAlaSerLYrGLYrGLYrArgProSerSerGLYrLYrILEuAlaLEuHisPheGLY 317
 Db 923 CCGCGCCGAGAAAGGAGAGAGCAAAAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 982
 Qy 318 ProProAsnAlaProLEuAsnArgLYrGLY-----LEuValSerProGINSerProGIN 335

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Db 983 GGCGCA---GCTGAGGTCAAGAGAGAGGTTCCAGCTGGAGAACGAGAGGCCCCGAG 1039
Qy 336 LysSerAspCysAlaInProAnserProThr-----GluAlaCysSerSer-Ly 351
Db 1040 GAAAGACGAGATATGAGATGACGGGCGACAGACTCGGGGAGAGAGCTCGGCTCGAGGCC 1099
Qy 351 AaenAlaCysAlaLeuGlnAlaSerGlySerProAlaLysSerProThrAspProLy 371
Db 1100 CGGGGCTGCTCGAGGACCTTACGGGACCGGACCGGACCTTACGGCTCCTGTC 1159
Qy 371 AaLysSerTrpLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 391
Db 1160 ATCCACAGATGCGAGG-----ACTGTGGAGAGAGGTTTCAAGCAGCGGGGAG 1207
Qy 391 sProGlyGlyProGluGlnAlaGluLysLysLysLysLysLysLysLysLysLysLys 410
Db 1208 TTCAAGGCGACATCCGATCCACAGGGGAGAGAGGCTTCTGTGCGGGAGTGGAG 1267
Qy 411 ----ProProAlaCysAlaInProAnserProThr-----GluAsnLeuAspLeuGln 427
Db 1268 AAGGCTTTTCCAGCCGGCGCGGTGCAAGGCCCATGAGAGAGAGAGAGAGAGAGAG 1327
Qy 427 rProThrLysLeuSerAlaSerGlyLysAspSerThrLysProGlnAlaSerArgLeu 447
Db 1328 CCTTACGCGCTGCGAGAGTGGGAGAGAGCTACC-----GCCCTCATCAGGCTG 1375
Qy 447 AaenAlaLysAspSerMetThrGlySerProArgSerSerSerSerSerSerSer 467
Db 1376 CTGAAGCTGCACAGAGAGGCGGCACTCGGCGAGAGCGGCTTCAAGCTC---GCGAGAGCTGC 1432
Qy 467 oLeuTyMetHisAspProLysCysThrSer-----CysGlySerGly 481
Db 1433 GCGAAGCTCTTCAACCTCGGCGACCTCAAGGGCAGCAGCTGTGTCACAGCGGAG 1492
Qy 481 nSerProGlnHisAlaGluMetCysLeuHisThrAlaGlyProThrPheAlaGlu---- 499
Db 1493 AAGCCCTTAC-CAGTGCAGTACTATGC-----GGCGGCTCTTCTCCAGCCCA 1539
Qy 500 -----GluMetGlyGluThrGlnSerGlyLysSerAspSerSer 513
Db 1540 TTCCAGATGCGGCACTGTGAGACCAAGCAGCAGAGAGAGAGAGAGAGAGAGAG 1599
Qy 513 sGlu-----As 515
Db 1600 CGACAGAGAGTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1659
Qy 515 nGlyAlaPhePheCysAsnGlyCysAspCysArgPheSerGlnGlnAlaSerLeuLys 535
Db 1660 CGGGCCCTTCAAGTGCAGAGAGTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1719
Qy 535 gHisThrLeuGlnThrHisSer---AspLysProTyrLysCysAspArgCysGlnAla 554
Db 1720 GCAC---CTTCGATTCACAGCGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1776
Qy 554 rPheArgTyrLysGlyAsnLeuAlaSerHisLysThrValHisThrGlyGluLysPro 574
Db 1777 GTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1836
Qy 574 rArgCysAsnLysCysGlyAlaGlnPheAsnArgProAlaAsnLeuLysThrHisThr 594
Db 1837 CCAAGTGTGATGTGGGTAAAGGCTTCAACAGAGAGAGAGAGAGAGAGAGAGAGAG 1896
Qy 594 gLysHisSerGlyGluLysProTyrLysCysGlnThrCysGlyAlaLysPheValGln 614
Db 1897 CCAAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1956
Qy 614 LAlaHisLeuArgAlaHisValLeuHisThrGlyGluLysProTyrProCysGly 634
Db 1957 CAGCAGTGTGGCAGATATATTCGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2016
Qy 634 eCysGlyThrArgPheArgHisLeuGlnThrLysSerHisLeuArgHisThrGly 654
Db 2017 GTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2076

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Qy 654 YGluLysProTyrHisCysGlyLysCysAsnLeuHisPheArgHisLysSerGlnLeuArg 674
Db 2077 AGAGAGAGCTTACCTGTGTGATGATGAGTGGGCTTCAACCGGGATGAGAGAGAGAG 2136
Qy 674 gLeuHisLeuArgGlnLysHisGlyAlaLeuThrAsnThrLysValGlnTyrArgVal 694
Db 2137 CTCCAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2182
Qy 694 rAlaThrAspLeuProProGlu 701
Db 2183 -----CTGAGAGCCGAG 2194

RESULT 14
US-10-122-851-309
/ Sequence 309, Application US/10122851
/ Publication No. US20050239060A1
/ GENERAL INFORMATION:
/ APPLICANT: Tang, Y. Tom
/ APPLICANT: Liu, Chenghua
/ APPLICANT: Asundi, Vinod
/ APPLICANT: Ren, Feiyang
/ APPLICANT: Drmanac, Radoje T.
/ TITLE OF INVENTION: Novel Nucleic Acids and
/ TITLE OF INVENTION: Polypeptides
/ FILE REFERENCE: 784CIP2BDV3
/ CURRENT APPLICATION NUMBER: US/10/122,851
/ PRIOR FILING DATE: 2002-04-12
/ PRIOR APPLICATION NUMBER: 09/620,312
/ PRIOR FILING DATE: 2000-07-19
/ PRIOR APPLICATION NUMBER: 09/552,317
/ PRIOR FILING DATE: 2000-04-25
/ PRIOR APPLICATION NUMBER: 09/488,725
/ PRIOR FILING DATE: 2000-01-21
/ NUMBER OF SEQ ID NOS: 1104
/ SOFTWARE: pc_fl_genes version 1.0
/ SEQ ID NO 309
/ LENGTH: 2769
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (248) ..(2659)
US-10-122-851-309

Alignment Scores:
Pred. No.: 1,74e-47 Length: 2769
Score: 621.50 Matches: 205
Percent Similarity: 41.0% Conservative: 102
Best Local Similarity: 27.4% Mismatches: 288
Query Match: 16.4% Indels: 154
DB: 9 Gaps: 25

US-10-755-889-18 (1-706) x US-10-122-851-309 (1-2769)
Qy 9 lLeGlnPheThrArgHisAlaSerAspValLeuLeuAsnLeuAsnArgLeuArgSerArg 28
Db 248 ATGAGATTTTCCCGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 307
Qy 29 AspIleLeuThrAspValValIleValIleValIleValIleValIleValIleValIle 48
Db 308 GGGCTTCTGTGATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 367
Qy 49 ValLeuMetAlaCysSerGlyLysPheTyrSerIlePheThrAspGlnLeuLysCysAsn 68
Db 368 GTGCTGCGCGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 415
Qy 69 LeuSerValIleAsnLeuAspProGluIleAsnProGluIlePheCysIleLeuLeuAsp 88
Db 416 AAGAGAGTGTGATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 472
Qy 89 PheMetTyrThrSerArgLeuAsnLeuArgGlyLysAsnIleMetAlaValMetAlaThr 108

```


APPLICANT: HAFALIA, April J.A.; HONGBELL, Cynthia D.;
APPLICANT: ISON, Craig H.; KHAN, Farrah A.;
APPLICANT: LAL, Preeti G.; LEE, Ernestine A.;
APPLICANT: LEE, Sally; LEE, Soo Yeun;
APPLICANT: LI, Joana X.; LU, Dying Aina M.;
APPLICANT: LU, Yan; LEHR-MASON, Patricia M.;
APPLICANT: NGUYEN, Daniel B.; RAMKUMAR, Jayalaxmi;
APPLICANT: SPRAGUE, William W.; TANG, Y. Tom;
APPLICANT: THANGAVELU, Kavitha; THORNTON, Michael B.;
APPLICANT: TRAN, Vylen K.; CHAMLA, Narinder K.;
APPLICANT: WARREN, Bridget A.; XU, Yuming;
APPLICANT: YAO, Monique G.; YUE, Henry;
APPLICANT: YUE, Hubbin; ZEBARJADIAN, Yeganeh
TITLE OF INVENTION: NUCLEIC-ACID ASSOCIATED PROTEINS
FILE REFERENCE: PF-1146 USN
CURRENT APPLICATION NUMBER: US/10/486, 977
CURRENT FILING DATE: 2004-02-17
PRIOR APPLICATION NUMBER: PCT/US02/25829
PRIOR FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: US 60/313,111
PRIOR FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: US 60/314,682
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/314,756
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/315,105
PRIOR FILING DATE: 2001-08-27
PRIOR APPLICATION NUMBER: US 60/316,751
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/316,856
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/328,185
PRIOR FILING DATE: 2001-10-05
NUMBER OF SEQ. ID NOS: 66
SOFTWARE: PERL Program
SEQ ID NO 45
LENGTH: 3451
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: incycle ID No: 3217430CB1
US-10-486-977-45

Alignment Scores:
Pred. No.: 2,99e-42 Length: 3451
Score: 567.00 Matches: 199
Percent Similarity: 39.1% Conservative: 95
Best Local Similarity: 26.5% Mismatches: 243
Query Match: 14.9% Indels: 215
Gaps: 26
US-10-755-889-18 (1-706) x US-10-486-977-45 (1-3451)
14 HislaserapValleuleuLeuLeuAnArgSerArgAplleuThrAsp 33
Db 150 CACAGCGCCATCGCTCCAGCACTGACAGAGCAAGCCTTGCGTTC 209
34 ValValleValValSerArgGluGlnPheArgAlaHisLysThrValleuMetAlaCys 53
Db 210 TGTATGTTGGTGAAGAGAGCTGCTTTAAAGCCGATTAAGATGCTGGCAGCATTC 269
54 SerGlyLeuPheTyrSerIlePheThrAspGlnLeuLysCysAsnLeuSerValIleAsn 73
Db 270 AGCAGATATTTCAGAGCCCTTTTCAGATTTCTTCAAGCCAGAAATGATGTTTTTCAC 329
74 LeuAspProGluIleAsnProGluGlyPheCysIleLeuLeuAspPheMetTyrThrSer 93
Db 330 TTGAATGTTAA---AATGTCAGTGGCATAGGAGAGATCTTGACCTTACATCTTCT 386
94 ArgLeuAnLeuArgGluGlyAsnIleMetAlaValMetAlaThrAlaMetTyrLeuGln 113
Db 387 CATCTAGATCTTACACGACCAATATATCAAGTAAATGCTGGACACAGCAGATGTTTCCA 446

MetGluHisValAlaSerThrCysArgLysPheIleLysAlaSerGluAlaGluMetVal 133
Db 447 GTTCAAAATGTTCTAGCTGTGTGCACACATTTTAAATATACGCC----- 491
134 SerAlaIleLysProProArgGluGlnLubPheLeuAsnSerArgMetLeuMetProGlnAsp 153
Db 492 ACTGATGATCAGGCCACTGCGC-----ATGGCT----- 518
154 IleMetAlaTyrArgGlyArgGluValAlaGluAsnAnLeuProLeuArgSerAlaPro 173
Db 518 ----- 518
174 GlyCysGluSerArgAlaPheAlaProSerLeuTyrSerGlyLeuSerThrProProAla 193
Db 519 ---TGTAAATGATCAATG-----TCTGCAAAAGCACCCTG---ACCCAGATGCC 563
194 SerTyrSerMetTyrSerHisLeuProValSerSerLeuLeu---PheSerAspGluGlu 212
Db 564 ACTTGTTATTCAGTGAAGAAATACCCCTCATTTTACCTGCAGGAATGTTTCAGCAATGCA 623
213 PheArgAspValArgMetProValAlaAsnProPheProLysGluArgAlaLeuProCys 232
Db 624 CAGCAGAAACAAACGTTGATGAATCGCATCCG-----CATGCTTCACCAATCA 671
233 AspSerAlaArgProValProGlyLutyrSerArgProThrLeuGluValSerProAsn 252
Db 672 GTTAATCGCATCACTCCGACAGTGAATCTCAAAACAGCCTCGATATCTTCAATGCG 731
253 ValCysHisSerAsnIleTyrSerProLysGluThrIleProGluGluAlaArgSerAsp 272
Db 732 ACCTGC-----ACAGAACTGCCCTTTCAAA---CAGCCAAAT 764
273 MetHisTyrSerValAlaGluGlyLeuLysProAlaAlaProSerAlaArgAsnAlaPro 292
Db 765 TACTATTCACAAATC-----AGAAAC----- 785
293 TyrPheProCysAspLysValSerLysGluGluArgProSerSerGluAspGluIle 312
Db 786 ---TTTACAGTAACAGATACCATTAACAGAGCTGCTCCAGTCAGAGAGATGTT 842
313 AlaLeuHisPheGluProProAsnAlaProLeuAsnArgLysGlyLeuValSerProGln 332
Db 843 -----GAGAGCCTTTTGTCTTTCAGACACCTTACAGACCTTACCGAGTAGAG 890
333 SerProGlnLysSerAspCysGlnProAsnSerProThrGluAlaCysSer---SerLys 351
Db 891 AGC-----CAGCCT-----TGCTGTCAATCAT 914
352 AsnAlaCysIleLeuGlnAlaSerGlySerProProAlaLysSerProThrAspProLys 371
Db 915 TCTGAATGATCTCTGAGTCT-----CCGAGCAGCTTACCTTCC----- 953
372 AlaCysAsnTrpLysTyrLysPheIleValLeuAsnSerLeuAsnGlnAsnAlaLys 391
Db 954 -----AAGCTTCGCGCCAGCCTGTGAAT 977
392 ProGlyGlyProGluGlnAlaGluLeuGlyArgLeuSerProArgAlaSerThrAlaPro 411
Db 978 GACTCTGCCCAACACCT-----GAGTCAGAC 1004
412 ProAlaCysGlnProProMetGluProGluAnLeuAspLeuGlnSerProThrLysLeu 431
Db 1005 GCCACATGCCAACACCTGTCAAG-----CAGATGAGGCTCAAAAG 1046
432 SerAlaSerGlyLubAspSerThrIleProGlnAlaSerArgLeuAsnAnIleValAsn 451
Db 1047 GCCAT-TCACTGAAAGAACTCAATTCTGAAATGACAGAAATACGC----- 1093
452 ArgSerMetThrGlySerProArgSerSer-SerGluSerHisSerProLeuTyrMetHis 471
Db 1094 -----AGAGCAAGTATCTGAA----- 1109

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QY 471 sPProTylsCyethrSerCysglSerGlnSerProGlnHisAlaGluMetCysLeuH1 491
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Db 1110 -----CCCAAG-----TCAGATGATGTTTGAACAAAGAGTTGA 1144
QY 491 sThrAlaGlyProThrPheAlaGluGluMetGlyGluThrGlnSerGluTyrSerAspSe 511
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Db 1145 ATCTGCTAGTAAATAATCCCTAGAGAAAGCTAGACAGCCAAAGTCTGAAGAAAAGAAAG 1204
QY 511 r-----SerCysgluAenGlyAlaPhePheCysaenGluCysaPyrCysaPyrph 527
    |||||
Db 1205 TGAAGAGTGTGTGATGTTGAGAAAT-----TTAATTGCAATTAGTAGAGAGAGAGGCC 1258
QY 527 eSerGluGluAlaSerLeuLysArgHisThrLeuGlnThrHisSerAspLysProTyrLys 547
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Db 1259 TGAAGACCCGGCTGCTGCGAAGACCAAGTCCAGACACTTCAGTCCAGAGACAAATAGCC 1318
QY 547 sCyAspArgCysgluAlaSerPheArgTyrLysGlyAsnLeuAlaSerHisLysThrVa 567
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QY 567 lHisThrGlyGlyLysProTyrArgCysAsnHisCysglYAlaGlnPheAsnArgProAl 587
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Db 1379 TCATACAGGTGAGAAACCTTTTGAATGTAACATTTGTGGAAACATTTCTCTCAGGACAG 1438
QY 587 aAenLeuLysThrHisThrArgGlnHisSerGlyGlyLysProTyrLysCysgluThrCy 607
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QY 607 sGlyAlaArgPheValGlnValAlaHisLeuAlaHisValLeuLeuHisThrGlyG1 627
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QY 627 uLysProTyrProCysgluLeuLeuCysglYThrArgPheArgHisLeuGlnThrLeuLysSe 647
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QY 647 r-----647
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QY 647 -----647
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QY 648 -----HisLeuArg11 651
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Db 1739 CTGCTTCGCTGCGGGAATGTTTGGGGGATCAGGTGACCTCCGACAGGCATGTCCGCAC 1798
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QY 671 rGlnLeuArgLeuHisLeuArgGlnLysHisGlyAla-1LeThrAsnThrLysValGlnT 691
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Db 1859 GGTGCTCCGGCGGCGCAAGAGAGATGCACTGCAAAAGCTGTGACGAGAGCCAGATGCT 1918
QY 691 yArgValSerAlaThrAspLeuProPro 700
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Db 1919 GAGGAGCTCAGCCCAAGCATGAGACCT 1947
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Job time : 1480 secs

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Qy	651	IleHisThrGlyGluLysProTyrHisCysGluLysCysAsnLeuHisPheArgHisLys	670
Db	2528	GTTTCACACAGGAGAGAGCCCTTATGAATGACCTGAATGTGGGAAGGCTTTATAGTCAGACG	2469
Qy	671	Ser-----GlnLeuArgLeuHisLeuArgGlnTyrHisGlyAlaIleThrAsn	686
Db	2468	TCATCCCGTGCTCAGCATCTTGAGACTTTCACAGGCCAGAAGCCCTATGCATGTGTGTAA	2409
Qy	687	ThrLysValGlnTyrArgValSerAlaThr	696
Db	2408	TGTGAGAAGGCATTTCAGAAACAAATCATCA	2379

Search completed: March 2, 2006, 04:05:09
Job time : 630 secs

Db	3590	GAATGTGAGAAACCTTCCACGAGGCTCATCT	::: :::: ::::	ProCysGlu1Leu1CysGlyThrArgPheArgHisLeuGlnThrLeu1Leu1SerHisLeuArg	3540
Qy	316	PheGluProProAsnAlaProLeuAenArgLysGlyLeuValSerProGlnSerProGln	::: :::: ::::	ProGlnSerProGlnSerProGln	335
Db	3539	ATTCTACTCGGAGAGAAACCATATGAGTGTAA--GGACTGTGGAGAGCCCTTCAAC		CAGAG	3481
Qy	336	LysSerAspCysGlnProAenSerProThrGluAlaCysSerSerLysAenAlaCysIle	::: :::: ::::	CysIle	355
Db	3480	TCAACACTTGTCC-----AGACCACAGATATACACCCGGAGAAAACATATTTTGAAT		TTTGAAT	3428
Qy	356	LeuGlnAlaSerGlySerProProAlaLysSerProThrAspProLysAlaCysAenTrp	::: :::: ::::	CysAenTrp	375
Db	3427	GTAAGGAATGTAGGAAGCCTTCAGCCAAATGTACATC-----TTATTCAACATC		TTATTCAACATC	3377
Qy	376	LysGlyTyrLysPheIleValLeuAenSerLeuAenGlnAenAla-----LysProGly		LysProGly	393
Db	3376	AAAGAAATTC---ATACTGGAGAAAACCATATATAATGTAGGAGTGTAGAAAAGCCCTTCA		AGCCCTTCA	3320
Qy	394	GlyPro-----GluGlnAlaGluLeuGlyArg-----LeuSer		LeuSer	404
Db	3319	GCACGCTGCACACCTTGTCTCAGCATCAGAGAATTATCTATCGGGAGAGCCCTTATAAT		CTTATAAT	3260
Qy	405	ProArgAlaTyrThrAlaProProAlaCysGlnProProMetGluProGluAenLeuAsp		LeuAsp	424
Db	3259	GTAAGGAATGTGCAAGCCTTCAGTGATCGCTCTTGTGCC-----GAC		GAC	3212
Qy	425	LeuGlnSerProThrLysLeuSerAlaSerGlyLysAspSerThrIleProGlnAlaSer		AlaSer	444
Db	3211	ATCAGAGGTGTACA-----CTGGCAAAAGACGTCAGTAATGTTGAATGTGGGA		GTGGGA	3161
Qy	445	ArgLeuAenAenIleValAenArg--SerMetThrGlySerProArgSerSerSerGlu		SerSerSerGlu	463
Db	3160	AAGCTTTCAGGCAGAACACATCGCTTATCGTCACTGGAGATAT--TATCACATGGGAG		ATGGGAG	3102
Qy	464	SerHisSerProLeuTyrMetHisProProLysCysThrSerCysGlySerGlnSerPro		SerGlnSerPro	483
Db	3101	AAA-----CCCTTTGACTGCATCGACTGTGGAGGCCCTTCAGC		CTTCAGC	3063
Qy	484	GlnHisAlaGluMetCysLeuHis-----		-----	491
Db	3062	GATCACATAGGACTTATTTCAGCACAGGAGGATTCATCTCGAGAGAAACCTTCAAAATGT		CTTCAAAATGT	3003
Qy	492	--ThrAlaGlyProThrPheAlaGluMetGlyGluThrGlnSerGluTyrSerAsp		SerAsp	510
Db	3002	AATGTGTGGGAAAACCTTCAGC-----TACGGCTCATCCCTGACCGCTCCATCAGAGA		CTCCATCAGAGA	2949
Qy	511	SerSerCysGluAenGlyAlaPhePheCysAenGluCysAspCysArgPheSerGluGlu		SerGluGlu	530
Db	2948	ATTCACACAGGAGAGAAACCATATGATGTGACATCTGTGGAAAGCCTTCAGCCATCAT		CTTCAGCCATCAT	2889
Qy	531	AlaSerLeuLysArgHisThrLeuGlnThrHisSerAspLysProTyrLysCysAspArg		CysAspArg	550
Db	2888	GCCTCACTCACCCAGCAACCAAGAGTGCATCTCTGGAGAGAAAGCCTTACCAATGCAGGAA		ATGCAGGAA	2829
Qy	551	CysGlnAlaSerPheArgTyrLysGlyAenLeuAlaSerHisLysThrValHisThrGly		ThrValHisThrGly	570
Db	2828	TGTGGAAAAGCTTTCAGGCAGAGCATACACCTTCTAGCCATCTGAGGATCCATCTGGGA		CTGAGGATCCATCTGGGA	2769
Qy	571	GluLysProTyrArgCysAenIleCysGlyAlaGlnPheAenArgProAlaAenLeuLys		ProAlaAenLeuLys	590
Db	2768	GAAAAACCTTATGAATGTAAAGGAATGTGAAAGCCTTTAGCATCATGTTACAGCTGGCT		TTTACAGCTGGCT	2709
Qy	591	ThrHisThrArgIleHisSerGlyGluLysProTyrLysCysGluThrCysGlyAlaArg		CysGlyAlaArg	610
Db	2708	ACTCATCAGAGAAATTCATCTACTGGAGAGAAACCTTATGAATGTAAAGGAATGCGGAAAGCC		ATGCGGAAAGCC	2649
Qy	611	PheValGlnValAlaHisLeuArgAlaHisValLeuIleHisThrGlyLysProTyr		ThrGlyLysProTyr	630
Db	2648	TTCAACCGAGGGACATCTTCGCACAGCACCATATAAATTCATCTGGAGAGAAACCTTAC		CTGGAGAGAAACCTTAC	2589
Qy	631	ProCysGlu1Leu1CysGlyThrArgPheArgHisLeuGlnThrLeu1Leu1SerHisLeuArg		SerHisLeuArg	650

QY 285 aProSerAlaArgAsnAlaPro-----TyrPheProCysAspLysAlaSerLy 301
 Db 374 CCCAAATGCAATTTTTCACCCCATCTCAGTATGATTTTGGTGGCCGCAATTTCA----- 428
 QY 301 sGIUGLUAGrProSerSerGluAspGluIleAlaLeuHisPheGluProProAsnAl 321
 Db 429 -----CATTCCTCACCCCGAATAATG 448
 QY 321 aProLeuAsnArg-----LysGlyLeuValSe 330
 Db 449 CATGCCAGACCGTGTCTTTCAGAGCTGTAACTTTGAGATGATGCTGTACTTCA 508
 QY 330 rProGlnSerProGlnLysSerAspCysGlnProAsnSerProthGluAlaCysSerSe 350
 Db 509 TCCGGAAGAGGTGGAAGCGTTTGGAACTGCTCAGAGGAGCCTTATGAGATGATGATGC 568
 QY 350 r-----LysAsnAlaCysGlyLeuGlnAlaSerGlySerProProAlaLys----- 365
 Db 569 TGGAGAAATTACCGGAATGTGTCTCACTGATGCTG-AGAACCAGACTGAAATGATCA 627
 QY 366 -----SerProThrAspProLysAlaCysAsnTrpLysLysLys-----Ph 380
 Db 628 GAAATTTCTGAGACACAAAGATCAATGGGCTCTACTGGAGATTTCAAAAGATATT 687
 QY 380 eIleValLeuAsnSerLysAsnGlnAsnAlaLysProGlyGlyProGluGlnAlaGlu 400
 Db 688 TCTCAGGGTCTCAAGTTTAAAG-----AGCCTAAGAACAGAGAGTCACTGAA 738
 QY 400 uGlyATrGLeuSerProArgAlaTrpThrAlaProProAlaCysGlnProProMetGluP 420
 Db 739 AGGCCCTGGGGA-----ACTCC-CCT-----GQ 761
 QY 420 oGluAsnLeuAspLeuGlnSerProThrLysLeuSerAlaSerGlyLysAspSerThrI 440
 Db 762 AGAAAGACTGAGACGAAATGCCAGATTTTGGTCAAGTACAGCTTGAGAGAAAGCTAAC 821
 QY 440 eProGlnAlaSerArgLysLeuAsn-----AsnIleValAsnArgSerMetThrGlySerP 458
 Db 822 CCCAGAGGAGAGAGAGGAGAAATATATATGATTTTGGAGACAGCTTCACTGATTC 881
 QY 458 oArgSerSerSerGlnSerHisSerProLeuTrpMetHisProProLysCysThrSerCy 478
 Db 882 CAACCTTATCTCATCAGAGACTCCCTGGGAGAGACAGCCCATTAAGTATGAATG 941
 QY 478 sGIY-----SerGlnSerProGlnHisAlaGluMetCysLeuHisTh 492
 Db 942 TAGCAAGAGCTTAAATCACTTCAAGCTTATTCATCAGACAGAG-----ATCCAC 995
 QY 492 rAlaGlyProThrPheAlaGluGluMetGlyGluThrGlnSerGluTrpSerAspSerSe 512
 Db 996 TGGGGAAGAACCTAT-----GATGTATATGATGTGGGAAGGCTTCCAGCCAGAGCTC 1049
 QY 512 r-----CysGluAsnGlyAlaPhePheCysAsnGlyCy 523
 Db 1050 ACACCTTATTCACATCAGAGAAATCCACTGAGGAGAAACCTTATTAAGTATGATG 1109
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 Db 1170 GAAACCTATGATGATGATGATGTGGGAAGACCTTCACTGAGAGCTCCACCTCAACCA 1229
 QY 563 rHisLysThrValHisThrGlyGluLysProTrpArgCysAsnIleCysGlyAlaGlnP 583
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 Db 1290 CAGCAGAGAGCTCAACCTTATTCACATCAGAGATCCACTGAGAGAAACCTTATGA 1349

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 US-10-750-185-44166/c
 ; Sequence 44166, Application US/10750185
 ; Publication No. US20050260603A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MMI GENOMICS, INC.
 ; APPLICANT: DENISE, Sue K.
 ; APPLICANT: KERR, Richard
 ; APPLICANT: ROSENFELD, David
 ; APPLICANT: HOLM, Tom
 ; APPLICANT: BATES, Stephen
 ; APPLICANT: FANTIN, Dennis
 ; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
 ; FILE REFERENCE: MM1100-2
 ; CURRENT APPLICATION NUMBER: US/10/750,185
 ; CURRENT FILING DATE: 2003-12-31
 ; PRIOR APPLICATION NUMBER: US 60/437,482
 ; PRIOR FILING DATE: 2002-12-31
 ; NUMBER OF SEQ ID NOS: 64922
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 44166
 ; LENGTH: 4305
 ; TYPE: DNA
 ; ORGANISM: Bovine 19866880546157
 US-10-750-185-44166
 Alignment Scores:
 Pred. No.: 8,466-21 Length: 4305
 Score: 462.00 Matches: 147
 Percent Similarity: 42.0% Conservative: 59
 Best Local Similarity: 30.0% Mismatches: 214
 Query Match: 12.2% Indels: 73
 DB: 8 Gaps: 18
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 QY 261 ProLysGluThrIleProGluGluAlaArgSerAspMet-----HisTrpSerVal 277
 Db 3680 CACAGCTCAGATGAAAAAATTTTCCAGAAATTCATGATGATTAATAACAGAAAGAT 3621
 QY 278 AlaGluGlyLeuLysProAlaAlaProSerAlaArgAsnAlaProTrpPheProCysAsp 297
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Qy     401 YATgLeuSerProAaGlaTyThAlaProProAlaCyGlnProPomeGluProG1 421
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Qy     575 gCyAaenLLeCyGlnGlyAlaGlnPheAaAaThProAlaAaenLeuLysThrHisThrAlaG1 595
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Db     595 eHisSerGlyGluLysProTyThCyGlnThrCyGlnGlyAlaAaPheValGlnValAl 615
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Db     635 eGlyThrAaPheAaThLeuGlnThrLeuLysSerHisLeuAaG11eHisThrGlyG1 655
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Qy     655 uLysProTyThHisCyGlnLysCyAaenLeuHisPheAaThLysLysSerGlnLeuAaGLe 675
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      1980 GCATTAAGG 1989

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RESULT 14
US-11-072-512-816
; Sequence 816, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KETICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 816
; LENGTH: 2634
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-072-512-816

Alignment Scores:
Pred. No.: 4,9e-21 Length: 2634
Score: 462.50 Matches: 162
Percent Similarity: 39.9% Conservative: 70
Best Local Similarity: 27.9% Mismatches: 258
Query Match: 12.2% Indels: 93
Gaps: 21

US-10-755-889-18 (1-706) x US-11-072-512-816 (1-2634)
Qy      172 AlaProGlyCyGlnSerAaGlaPheAlaProSerLeuTySerGlyLeuSerThrPro 191
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     20 TCCCGGATGTGTGGTCTGTGACAGGGTCCAAAGGCGCTGTGCTC--GTGCGGCTCC 76
Qy     192 ProAlaSerTySerMet-TyrSerHisLeuProValaSerSerLeuPheSerAaPgl 211
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      77 CCAATATCTGTGCTCTGCCCCCAGGCTCTTCTTCAAAAGTCTGCTTCCGACAA 136
Db     211 uGlnPheAaThAaPValaAaPmetProValaAlaAaPProPheProLysGlnAlaLeuPr 231
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      137 GAGACAGCTGGGAGATGAGATGTTGCGCGCTGCTTAAGGCAAGTCCAGGTGAG 196
Qy     231 oCyAaPserAlaAaPProValaProGlyGluTy-----SerAaPProThrLeuG1 248
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      197 CTGGGTCCGTTATCTTTTCCATTTCTGTCGCAATGACATCCATCCATTCAGAGC 256
Db     248 uValSerProAaenAl-----CyHisSerAaenLeuTySerProLysGluThr11 265
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      257 TTTAACCTTATCTCTCCATCAGAGCCCAAGTGTCTGTCTGCGTGAATGCGAGACCTC 316
Qy     265 eProGlnGlnAlaAaPserAaPmetHisTySerValaAlaGlnGlyLeuLysProAlaAl 285
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      317 ACCTTCTATCTTGAACCTGTGTCTCTTCTCCACCCGTGCTCCCTT---CTCCCTT 373

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Oy 339 CysGlnProAsn-----SerProthrglnAla 347
    :|||
Db 412 AGAGGCGCCAGAGGCTCTGAAGTTCTGAGACTGGCCGTTACTTCTCCCGAGAGAGTGG 471
Oy 348 CysSerSerlysaAnaCyrlleuGlnAlaSerGlySerProProAlaLysSerPro 367
    :|||
Db 472 -----GGCTGCTCGCGGCCCGCCAGAGGCGCC----- 498
Oy 368 ThrAspProLysAlaCysAsnTrpLysLysLysPheLleValLeuAsnSerLeuAsn 387
    :|||
Db 499 -----CTGTACCGGAGCGGTGATCGCGAGACCTACCGT 531
Oy 388 GlnAsnAlaLysProGly-----GlyProGlnGlnAlaGluLeuGlyArgLeuSerPro 405
    :|||
Db 532 CACCTGGGCGCGCTCGGCTGGCGAGGTCACCAACAGACCTCTCATCTCTGTTGGAAAGA 591
Oy 406 ArgAlaLysThrAlaProProAlaCysGlnProProMetGlu-----ProGlnAsnLeuAsp 424
    :|||
Db 592 AACACCGATGACTGGAAACCGGCTGCTGATCCGAGAGTACCGGAGAGGCTTACA 651
Oy 425 LeuGlnSerProThryLysLeu-----SerAlaSerGlyLysLysSerThryLysPro----- 441
    :|||
Db 652 GTCCAGAGAAAGAACAGAACAGAAAGAGATGGGAGAAAGATATTCGCGCTTAA 711
Oy 442 GlnAlaSerArgLeuAsnAsnLleValAsnArgSerMetThryGlySer-----ProArg 459
    :|||
Db 712 GAGGACCCCGAAAGGAAAGGAGGCGGAGGCGGAGCCCAAGAACCCCGACGATTCCTAAG 771
Oy 460 SerSerSerGlySerLysSerProLeuLysLysLysLysLysLysLysLysLysLys 479
    :|||
Db 772 CAGACGTCGCGGCGCC-----CCCATCTGCTCGTACGTCGCGC 807
Oy 480 SerGlnSerProGlnHisAlaGluMetCysLeuHisSerThryAlaGly----- 494
    :|||
Db 808 TGTACTTCTCTGATCATCAGGCGCTGAGAGGACCAAGTGGCGCCGAGAACTTAAAAAG 867
Oy 495 -----ProThrPheAlaGluGluMetGlyLysLysLysLysLysLysLysLysLys 510
    :|||
Db 868 CTTTACCTTGGCCGAGACTGTGGCGCGCTTTCCTATCCATCCATCCGCTGTGATGATCAC 927
Oy 511 SerSerSerGlyLysAngly-----AlaPhePheCysAngLysCysAspCysArgPheSer 528
    :|||
Db 928 CGGGGGGACACTCGGAGAGTGGCCCTATGTTGTGACAGTGTGGAAACGTTTCTCC 987
Oy 529 GluGlnAlaSerLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 548
    :|||
Db 988 CAGCGCAAGAACTCTCCAGCAAGTGTATCCATCAGGGGAGAAAGCCCTATCACATGC 1047
Oy 549 AspArgCysGlnAlaSerPheArgLysLysLysLysLysLysLysLysLysLysLys 568
    :|||
Db 1048 CTTGACTGTGGTCTGCTCTCCGAGAGCGGCTTGGCCATCCAGCCGACACACACAC 1107
Oy 569 ThrGlyGlyLysProLysArgCysAsnLleCysGlyAlaGlnPheAsnArgProAlaAsn 588
    :|||
Db 1108 ACAAGTGAATAAACCCACACAGTGGCCCTAGCTGTGAGACGTGCTTCCCTACCCCTCGT 1167
Oy 589 LeuLysThryLysThryLysLysLysLysLysLysLysLysLysLysLysLysLys 608
    :|||
Db 1168 CTAAGCATCCACAGCGTACACACAGGAGAGAAAGCCCTACATCTGCTGAGTGGCAAC 1227
Oy 609 AlaArgPheValGlnValAlaHisLysLysLysLysLysLysLysLysLysLysLys 628
    :|||
Db 1228 CGCGGCTTCCGCGAGCGAGCGCCCTGCTATCCACAGCGCATCCACAGCGGAGAGAG 1287
Oy 629 ProLysProCysGlnLleCysGlyLysThryArgPheArgHisLysGlnThryLysSerHis 648
    :|||
Db 1288 CCTTACCCGCTGCGGAGCTGAGAGGCGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1347
Oy 649 LeuArgLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 668
    :|||
Db 1348 CGGGGTGTGCACTGTGGGAGAGGTCTCTATGCTGCGAGCACTGTGAGAGCGCGCTTCTCC 1407
Oy 669 HisLysSerGlnLeuArgLeuHis 676

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Db 1408 CAGCGAGACAGCTGCTCCAGCAC 1431
RESULT 12
US-11-072-512-693
/ Sequence 693, Application US/11072512
/ Publication No. US20060029945A1
/ GENERAL INFORMATION:
/ APPLICANT: ISOGAI, TAKAO
/ APPLICANT: SUGIYAMA, TOMOYASU
/ APPLICANT: OTSUKI, TETSUJI
/ APPLICANT: WAKAMATSU, AI
/ APPLICANT: SATO, HIROYUKI
/ APPLICANT: ISHII, SHIZUKO
/ APPLICANT: YAMAMOTO, JUN-ICHI
/ APPLICANT: ISONO, YUUKO
/ APPLICANT: HIO, YUKI
/ APPLICANT: OTSUKA, KAORU
/ APPLICANT: NAGAI, KEIICHI
/ APPLICANT: IRIE, RYOTARO
/ APPLICANT: TAMECHIKI, ICHIRO
/ APPLICANT: SEKI, NAOTIKO
/ APPLICANT: YOSHIKAWA, TSUTOMU
/ APPLICANT: OTSUKA, MOTYUKI
/ APPLICANT: NAGAHARI, KENJI
/ APPLICANT: MASUHO, YASUHIKO
/ TITLE OF INVENTION: Novel full length cDNA
/ FILE REFERENCE: 084335-0191
/ CURRENT APPLICATION NUMBER: US/11/072, 512
/ CURRENT FILING DATE: 2005-03-07
/ PRIOR APPLICATION NUMBER: US 60/350, 978
/ PRIOR FILING DATE: 2002-01-25
/ PRIOR APPLICATION NUMBER: JP 2001-379298
/ PRIOR FILING DATE: 2001-11-05
/ NUMBER OF SEQ ID NOS: 4096
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 693
/ LENGTH: 2241
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-11-072-512-693
Alignment Scores:
Pred. No.: 3,6e-21 Length: 2241
Score: 463.50 Matches: 122
Percent Similarity: 42.7% Conservative: 47
Best Local Similarity: 30.8% Mismatches: 139
Query Match: 12.2% Indels: 88
DB: 9 Gaps: 14
US-10-755-889-18 (1-706) x US-11-072-512-693 (1-2241)
Oy 347 AlaCysSerSerlysaAnaCyrlleuGlnAlaSerGlySerProProAlaLysSer 366
    :|||
Db 864 TCCTGTAGTGGCATCTCTCTCTGATCATCAAGGAGCTGATCTCT-----TTAACC 917
Oy 367 ProThrAspProLysAlaCysAsnTrpLysLysLysPheLleValLeuAsnSerLeu 386
    :|||
Db 918 CCAGCATTAACA-----TGTTC-----ATATCTTCTGTGAGCAGACCTTTA 962
Oy 387 AsnGlnAsnAlaLysPro-----GlyGlyProGlnGlnAlaGluLeuGlyArg 402
    :|||
Db 963 CACTCTTAAGCTTCAAGTATCTCTTATTTGAAACAGGAAAGAGCCCTGGATGGT--- 1019
Oy 403 LeuSerProArgAlaLysThryAlaProProAlaCysGlnProProMetGluProGlnAsn 422
    :|||
Db 1020 ---TGGCAGAGAGCTTAC-----AAGAGGCTGTGCTTCAGATCTGCA 1058
Oy 423 LeuAspLeuGlnSerPro-----ThryLysLeuSer 432
    :|||
Db 1059 ATCATGTGTGAACCAAGATTATCTTAAAGAGAAAGACTTATGAATAATGAATTATG 1118
Oy 433 AlaSerGlyLysLysSerThryLys-----Pro-GlnAlaSerArgLeuAsnAsnL 449

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Db      1102 AATGTAATTAATGCGCAAGCTCTT-----CAATGCAATGCA 1140
Qy      340  LnpProanserProthrGluAlaCyseSerSerLysAsnAlaCyvileuGlnAlaSerG 360
Db      1141 CACCT-----TACCAGACATCA 1158
Qy      360  LysEPro-ProAlaLysSerProThrAProLysAlaCyvAsnThrLys---LysEY 378
Db      1159 AGAATCCATCTGAGAGAAACCTTATGATGTAAGAAATGGCGAAGCTCTTCAGCGAC 1218
Qy      379  LysPhePheLysLeuLeuLeu-----SerLeuLeu 387
Db      1219 AAGTTTGTCTTACCAATCATCTAGAAATGACACCGGAGAGACCTTACAAATGTAAT 1278
Qy      388  GlnAsnAlaLysPro-GlyGly----- 394
Db      1279 GAATTTGGAGGCGCGAGCGGGGTGATCATAGAGTCAGAGATCGAGACATCTGGCTTA 1338
Qy      395  -----ProGlnGlnAlaGluLeuGlyArgLysSerProArgAlaThrAla 410
Db      1339 ACAAGGTGAACCCCATCTCTACTTAAATAATTAACAAATTAACCGGCGCGGGCGGCG 1398
Qy      410  APro-----ProAlaCyseGlnProProMetGluProGluAsnLeuAspLeuGlnSerP 428
Db      1399 GCCTGATGTCCTCCAGCTACTCGG-----GAGGCTGAGGCGAGAAATGGCTGAAC 1449
Qy      428  OThrLysLeuSerAlaSer-----G 435
Db      1450 CGGGAAGCGGAGCTTCAGTGAAGCGAGATTGGCCCATGTCAGTCCGAGTCCGCGCTGG 1509
Qy      435  YgluAspSerThrLysPro-----GlnAlaSerArgLeuAs 447
Db      1510 GCACAGAGAGAGACTCTCTCTCAAAAAAATAAATAAATAAATAAATAAATAAATAA 1569
Qy      447  nAsnIleValAsnArgSerMetThrGlySerProArgSerSerGluSerHisSerP 467
Db      1570 AATGTAATGAATGTGGCAAGTCTTC-ACTTACATTCACACCTTGACACAAATCAGAG 1628
Qy      467  oLeuTYMet-----HisProProLysCyvThrSerCyseGly-----SerGlnSe 482
Db      1629 AATACATCTCGAGAGAAACCTTACAAATGACATGACGTGGCAAGGTATTTAGTGA 1688
Qy      482  rProGlnHisAlaGluMetCyseLeu-----HisThrAlaGlyProTh 496
Db      1689 TCCG-----TGCTTACACGACATCAAGAGTTTCAACT----- 1722
Qy      496  rPheAlaGluGluMetGlyGluThrGlnSerGluTYSerAspSerSerCyseGluAsnG 516
Db      1723 -----GAGAGAGAG 1731
Qy      516  yAlaPhePheCyvAsnGlnCyvAspCyvArgPheSerGluAlaSerLeuLysArgH 536
Db      1732 -CCTTACAAATGTAATGAATGTGGCAAGCATTTAGAGACTGTTCAGCGCTTACTGCG 1790
Qy      536  eThrLeuGlnThrHisSerAspLysProTYLysCyvAspArgCyseGlnAlaSerPhe 556
Db      1791 TCTAATTAATTCACATCTGAGAGAAACCTTACAAATGTAAGAAATGTGCCAAGGTCT 1850
Qy      556  gTYrLysGlyAsnLeuAlaSerHisLysThrValHisThrGlyGluLysProTYArg 576
Db      1851 GCATAGATTATCCCTAAGCATATCAGAGATTTCATACCGAGAGAAACCTTACAGATG 1910
Qy      576  sAsnIleCyseGlyAlaGlnPheAsnProAlaAsnLeuLysThrHisThrArgLysH 596
Db      1911 TGAATGATGTGGCAGGAGCTTCACTGAAATTCAAACCTTGCAATATCAGAGATCCA 1970
Qy      596  eSerGlyGluLysProTYLysCyseGluThrCyseGlyAlaArgPheValGlnValAla 616
Db      1971 TACTGGAGAGAAACCTTACAAATGACATGATGTCACAAAGTCTTTAGTCACAATTCAC 2030
Qy      616  sLeuArgAlaHisValLeuLysThrGlyGluLysProTYProCyseGluLysCyseG 636
Db      2031 CTTTGCACGACATGAGCAATTCATCTGAGAGAGAGTCTTACAAATGCAATGATGTG 2090

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Qy      636  YThrArgPheArgHisLeuGlnThrLeuLysSerHisLeuArgLysHisThrGlyGly 656
Db      2091 CAAGGTCTTCAGCCCAAGATTATACCTTAATAAAGATGAGAAATTCATCTGGGAG 2150
Qy      656  eProTYrHisCyseGlyLysCyvAsnLeuHisPheArgHisLysSerGlnLeu----- 673
Db      2151 ACCGTACAGATCTCATGATGATGTGTAAGAGACTTCACTGAAATTCAAACCTGCA 2210
Qy      674  ---ArgLeuHisLeuArgGlnLys 680
Db      2211 TCACAGAAATCCATCTGAGAGAGAAA 2235

RESULT 11
US-10-517-151-3
; Sequence 3, Application US/10517151
; Publication No. US20060019252A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Yusuke
; APPLICANT: Furukawa, Yoichi
; APPLICANT: Oncotherapy Science, Inc.
; APPLICANT: The University of Tokyo
; TITLE OF INVENTION: Genes and Polypeptides Relating to Hepatocellular or
; FILE REFERENCE: 082379-000400US
; CURRENT APPLICATION NUMBER: US/10/517,151
; CURRENT FILING DATE: 2004-12-06
; PRIOR APPLICATION NUMBER: US 60/386,985
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: WO PCT/JP03/07070
; PRIOR FILING DATE: 2003-06-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2744
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (343)..(1845)
; OTHER INFORMATION:
US-10-517-151-3

Alignment Scores:
Pred. No.: 4,06e-21 Length: 2744
Score: 464.00 Matches: 135
Percent Similarity: 39.5% Conservative: 50
Best Local Similarity: 28.8% Mismatches: 205
Query Match: 12.2% Indels: 78
DB: Gaps: 14

US-10-755-889-18 (1-706) x US-10-517-151-3 (1-2744)
Qy      259  TYrSerProLysGluThrLys-----ProGluGluAlaArgSerAspMetHis 274
Db      112  TTTTCCCAAGAGCATCTTCCGCGCTTTCACCCAAAGTTCGGGCGAGAGTTTCTGAA 171
Qy      275  TYrSerValAlaGluGlyLeuLysProAlaAlaProSer-----AlaArg 289
Db      172  AACAGAAAGAGTTTCCGTTAGCCCGCGGGGAGCAAAATTCGAAATTCCTCGGCGCT 231
Qy      290  AsnAlaProTYrPheProCyvAspLysAlaSerLysGluGlnLysArgProSerSerG 309
Db      232  CCGGCGCACCTCAGCCCTGTGTCGCGAGGGGCTCTCGATCCAGAGGCGCGCAGCGCC 291
Qy      310  AspGluLysAlaLeuHisPheGlu-----Pro 318
Db      292  GAGGCGCGAGGCTTGACACGAGAGGCGCTGCGCGCGCTTCCTCGGCTCCATGCGCCA 351
Qy      319  ProAsnAlaProLeuAsnArgLysGlyLeuValSerProGlnSerProGlnLysSerAs 338
Db      352  CTTTGGCTCCGCTCCCTGCGAGGAGCAGAGAAAGGCCAGACCCAGTGGAAAGAGGCG 411

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QY	203	ValSerSerLeuLeuPheSerAspGluGluLeuArg-----AspValArg-----	217
Db	999	GTGATGATGTGGCAAGATCTTCAGAAAATAATTCATATTTGTTGAAGACACCAAAAGAGTC	1058
QY	218	-----MetProValAlaenProPheProPheGluArg	228
Db	1059	ACACTGCACAGAAACCTTACATATGTATGTAAATGGCAAGTCTTTAGTAAAGTTCC	1118
QY	229	AlaLeuProCybAbspSerAlaArgProValProGluTyrsArg-----Pro	245
Db	1119	ACCTTG-----CAGTTCATCAGGAATTCAACG	1148
QY	246	ThreGluValSerProAsnValCysHisSerAsnLeuTyrsProGluGluThrIle	265
Db	1149	GTGAAAAACCTTACAAATGATATCTGTGTGGAAATCC-TTAACT-----	1192
QY	266	ProGluGluAlaArgSerAaspMetHisTyrsValAlaGluGluLeuLysProAlaAla	285
Db	1193	---CAGCGTGTCATCTTAGACTTCACAGACTTCATACCTGAGAGAACCC-----	1243
QY	286	ProSerAlaArgAsnAlaProTyrsPheProCybAplySalaserGluGluGluArg	305
Db	1244	-----TTCAAATGATATGATGTGTGGCAAAACCTTTAAACGG	1279
QY	306	ProSerSerGluAaspGluAlaLeuHis-----PheGluProPro-----	319
Db	1280	AGCTCAAC-----CTCATGTGTACATCAGTAATTCATGCAGAAAGAACCAAT	1330
QY	320	-----AsnAlaProLeuAsnArgLysGluLeuVal--SerProGlns	333
Db	1331	AAATGTATGTATGTGGCAGGCACTTACAGACTATGATCAATCTTGATGTCACCGAGA	1390
QY	333	erProGluLysSerAaspCybGlnProAsnSerProThrGluAlaCysSerSerLysAsnA	353
Db	1391	ATCCACAGGAGAGAAAC-AATACAAATGCATGAATGTGGCAAGTCTTCAGTAAACG	1449
QY	353	IaCysIleLeuGln-----AlaSerGlySerP	362
Db	1450	TTCAAGCTTGTGAGGCATTCGACGAATTCACCTGTAGAGAAACCTTCAAAATGCATGA	1509
QY	362	roProAlaLysSerProThrAaspPro-LysAlaCysAsnTrpLysTyrsPheIle	381
Db	1510	ATGTGGCAAGCTTCAGTAAACGTTCAAGTTCAGT-----	1548
QY	382	ValLeuAsnSerLeuAsnGlnAsnAlaLysProGluGluAlaGluLeuGly	401
Db	1548	-----	1548
QY	402	ArgLeuSerProArgAlaTyrsThrAlaProProAlaCybGlnProMetGluProGlu	421
Db	1549	---GCATCAGAGAAATTCATACGACA-----GAA	1575
QY	422	AsnLeuAapLeuGln-----SerProThrLysSerAla	433
Db	1576	AACTTACAAATGCATTAATATGGCAAGGTGACAGTAAAGCATTCACATCTTGCAGTGCA	1633
QY	434	SerGluGluAaspSerThrIleProGluAlaSerArgLeuAsnAsnIleValAsnArgSer	453
Db	1636	TT-GGAGAA-----TTCATACCG---GGGAGAAAGCTTATTAATGCAATGAATGT-GGC	1684
QY	454	MetThrGlySerProArgSerSerArgLysSerHisSerProLeuTyrsMet-----His	471
Db	1685	AAAGTTTTCAGATACATTCACGACTTCGACGCTTCACAGAAATTCATCTGAGAGAAA	1744
QY	472	ProProLysCysThrSerCysGlySerGlnSerProGlnHisAlaGluMetCysLeuHis	491
Db	1745	CCTTACAAATGCAGAAATGTGGCAAGGCTTCAGTCAACATTCACAGTCTTCAGTGCAAT	1804
QY	492	Thr-----AlaGlyProThrPheAlaGluGluMetGlyGluThrGlnSer	506
Db	1805	CGGAGAAATTCATATCTGAGAGAAACCTTCAAAATGCAGAAAGATGTGGCAAGGTC-----	1855
QY	507	GluTyrsSerAaspSerSerCys-----GluAsnGlyAla	517

Db	1859	---	TTGATGACCGCTTACGCTTTGGCAAGGCATCGAGAAATTCACTCGAGAGAAAGCCT	1915
		:::		
Qy	518	Phe	heCyaaSenGluCyaaPerCyaaRgPheSeGluGluIaSeSerLeuLyaaRgHisThr	537
		:::		
Db	1916	TACAAAGTCAAAAGAAATGGCAAGGCTTTCAGTCAATGTTCACTCTTACAGTGCATCGG	1975	
Qy	538	Leu	GlnThrHisSerAspLeuProTyrLeuCyaaAspArgCyaaGlnIaSerPheArgTyr	557
		:::		
Db	1976	AGAATTCACTAGTGGAGAGAAACCTTACAATGCAATGCAATGCGCAAGGCTTACAGTCAG	2035	
Qy	558	Leu	SeGluAsnLeuIaSerHisValSerThrValHisThrGluGluLyProTyrArgCyaaAsn	577
		:::		
Db	2036	TATTCACATCTTGAAGGGCATCGAAGAGTTTCATCTCGAGAGAAACCATTCAAATGTCAT	2095	
Qy	578	Ile	CysGluAlaGlnPheAsnArgProAlaAsnLeuSerThrHisThrArgHisSer	597
		:::		
Db	2096	GAATGTGGCAAAAGCCTTTAATCAGGGCTCCACACTCAATAGACATCAGAGAAATTCATACC	2155	
Qy	598	Gly	GluLyProTyrTyrLeuCyaaGluThrCyaaGlyAlaArgPheValGlnValAlaHisLeu	617
		:::		
Db	2156	CGAAGAAACCTTCAAAATGCAATGCAATGTCGGAATTCCTTAATCAGCGTGCATCTT	2215	
Qy	618	Arg	AlaHisValLeuIleHisThrGlyGluLyProTyrProCyaaGluIleCyaaGlyThr	637
		:::		
Db	2216	AGACTTCATCAGACTGTTCACTAGAGACAGAACTTACAAATGTAATGAGTGGCAAA	2275	
Qy	638	Arg	PheArgHisLeuGlnThrLeuLySerHisPheArgHisLySerGlnLeu-----	657
		:::		
Db	2276	ACCTTTAAACGAGAGCTCAAACTTCACCTGACATCAGATGAATTCATGCAAGAAAGAAACCA	2335	
Qy	658	Tyr	HisCyaaGluLyProCyaaAsnLeuHisPheArgHisLySerGlnLeu-----	673
		:::		
Db	2336	TATAAATGTGATGGAATGGCAAGGTAATTCAGGCAATGTTCACTTGTAAATGACCAAG	2395	
Qy	674	Arg	LeuHisLeuArgGlnLyS 680	
		:::		
Db	2396	AGAAATCCACACTGAGAGAA 2416		
RESULT 9				
US-11-072-512-622				
Sequence 622, Application US/11072512				
Publication No. US20060029945A1				
GENERAL INFORMATION:				
APPLICANT: ISOGAMI, TAKAO				
APPLICANT: SUGIYAMA, TOMOYASU				
APPLICANT: OTSUKI, TETSUJI				
APPLICANT: WAKAMATSU, AI				
APPLICANT: SATO, HIROYUKI				
APPLICANT: ISHII, SHIZUKO				
APPLICANT: YAMAMOTO, JUN-ICHI				
APPLICANT: ISOINO, YUKIO				
APPLICANT: HIO, YURI				
APPLICANT: OTSUKA, KAORU				
APPLICANT: NAGAI, KEIICHI				
APPLICANT: IRIE, RYOTARO				
APPLICANT: TAMECHIKA, ICHIRO				
APPLICANT: SEKI, NAOHICO				
APPLICANT: YOSHIKAWA, TSUTOMU				
APPLICANT: OTSUKA, MOTOYUKI				
APPLICANT: NAGAHARI, KENJI				
APPLICANT: MASHIRO, YASUHIKO				
TITLE OF INVENTION: Novel full length cDNA				
FILE REFERENCE: 08435-0191				
CURRENT APPLICATION NUMBER: US/11/072,512				
PRIOR FILING DATE: 2005-03-07				
PRIOR APPLICATION NUMBER: US 60/350,978				
PRIOR FILING DATE: 2002-01-25				
PRIOR APPLICATION NUMBER: JP 2001-379298				
PRIOR FILING DATE: 2001-11-05				
NUMBER OF SEQ ID NOS: 4096				
SOFTWARE: PatentIn Ver. 2.1				
SEQ ID NO 622				

SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 1778
 LENGTH: 2110
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-11-072-512-1778

Alignment Scores:

Pred. No.:	16e-21	Length:	2110
Score:	468.50	Matches:	91
Percent Similarity:	48.4%	Conservative:	27
Best Local Similarity:	37.3%	Mismatches:	87
Query Match:	12.4%	Indels:	39
DB:	9	Gaps:	4

US-10-755-889-18 (1-706) x US-11-072-512-1778 (1-2110)

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Qy 472 ProProlyscysThrsercysgllyserglinsrproglinhlsalaglmetcysleuhs 491
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 932 CCTTACCAATGTGAAGATGTGGAAAGCCTTTACGAGTTCTCAATCTTACTACACAT 991
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 492 Thr-----AlaglyProThrPheAlaglmetcylglu-----Thr 504
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 992 AAAAAATTCATCTGAGAGAACCTTACATATGTGAAGATGTGGCAAGCCTTTTACC 1051
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 505 Gluserglu-----TyrSerasp 510
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1052 CAATCTTCACCTTACTACATATAGAAATTCATCTGAGAAAAACCTTACAAATGT 1111
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 511 SerSerCysgluaengly----- 516
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1112 GAAGAATGTGAAGAAGCTTTTAAACGATCCTCAAACTTACTGAACATTAATAACATTCAT 1171
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 517 -----AlaphePheCysaenglyCysaspCysargPheSeraglualaser 532
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1172 ACTGAGAGCAACCTTCAAAATGTGAGGAATGCGCAAGCTTTTAAACGATCCTCAAT 1231
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 533 LeuLyahrgHsThrLeuGlnThrHsSeraspLyProTylusCysaPargCysglN 552
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1232 CTTCAGGAACATGAGAAATTCATACCGAAGAAACCTTCAAAATGTGAAGATGTGGC 1291
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 553 AlaserPheargTylusglYAsnLeuAlaserHslystrValHsThrglYglulys 572
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1292 AAAGCTTTAAACCTCTCTGACCCCTTACTACATTAAGAAATTCACATCGAGAGAAA 1351
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 573 ProTylargCysaenlleCysglYAlaglnPheasnargProAlaasnLeuLyThrHs 592
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1352 CCTTACCAATGTGAAGATGTGGCAAGCTTTTAAACGATCCTCAAACTTACTGAACAT 1411
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 593 ThrargHsSeraglYglulysProTylusCysgluThrCysglYAlaargPheVal 612
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1412 AAGAACTTCATCTGGAAGAAACCTTCAAAATGTGAAGATGTGGCAAGCTTTTATTC 1471
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 613 GluValAlaHsleuArgAlaHsleuValleuHsThrglYglulysProTylusCys 632
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1472 CAATCTTCAAACTTACTGAAACATTAATAAAATTCATTTCTGAGAGATACCTTCAAGGT 1531
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 633 GluIleCysglYThrargPheargHsleuGlnThrleuLyserHsleuargHsleu 652
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1532 GAAGAATGTGCAAGCTTTTAAACATCTTCATCCTTACTACACATTAAGAATTCAT 1591
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 653 ThrglYglulysProTylusCysglulysCysaenlleuHsPheargHslySerGln 672
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1592 ACTGGGGGAAACCTTACAAATGTGAAGATGTGGCAAGCTTTTAAAGCGATCTCAAAA 1651
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 673 LeuargLeuHs 676
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1652 CTACTGAACAT 1663
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 8
 US-11-072-512-967
 Sequence 967, Application US/11072512
 Publication No. US20060029945A1

GENERAL INFORMATION:

APPLICANT: ISOGAI, TAKAO
 APPLICANT: SUGIYAMA, TOMOYASU
 APPLICANT: OTSUKI, TETSUJI
 APPLICANT: WAKAMATSU, AI
 APPLICANT: SATO, HIROYUKI
 APPLICANT: ISHII, SHIZUKO
 APPLICANT: YAMAMOTO, JUN-ICHI
 APPLICANT: ISONO, YUUKO
 APPLICANT: HTO, YURI
 APPLICANT: OTSUKA, KAORU
 APPLICANT: NAGAI, KEIICHI
 APPLICANT: IRIE, RYOTARO
 APPLICANT: TAMECHIKA, ICHIRO
 APPLICANT: SEKI, NAOHICO
 APPLICANT: YOSHITAKA, TSUTOMU
 APPLICANT: OTSUKA, MOTOKYU
 APPLICANT: NAGAHARI, KENJI
 APPLICANT: MASUHO, YASUHIKO
 TITLE OF INVENTION: Novel full length cDNA
 FILE REFERENCES: 084335-0191
 CURRENT FILING DATE: 2005-03-07
 PRIOR APPLICATION NUMBER: US 60/350,978
 PRIOR FILING DATE: 2002-01-25
 PRIOR APPLICATION NUMBER: JP 2001-379298
 PRIOR FILING DATE: 2001-11-05
 NUMBER OF SEQ ID NOS: 4096
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 967
 LENGTH: 3026
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-11-072-512-967

Alignment Scores:

Pred. No.:	3.55e-21	Length:	3026
Score:	465.50	Matches:	178
Percent Similarity:	40.1%	Conservative:	98
Best Local Similarity:	25.8%	Mismatches:	238
Query Match:	12.3%	Indels:	179
DB:	9	Gaps:	27

US-10-755-889-18 (1-706) x US-11-072-512-967 (1-3026)

```

Qy 84 CyslleuLeuaspPheMetTyrThrSerArgLeuasnleuargglulysaen---lle 102
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 609 TGCCCATGTGAACCAATCTTACTGTGTAAGATCAACATAGTCAAGGGAGATGTAGAAA 668
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 103 MetAlaValMetAlaThrAlaMetTyrLeuGlnMetGluHsValValaPthrCysarg 122
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 669 ACAATCTATTTGAAACACCTTACATCAAACTTTGAGTCAAGCTGCTGCAACTGAGA 728
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 123 LysPheIleLysAlaSerGluAlaGluMetValSerAlaIleLysProProArgglulN 142
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 729 AAGTTC-----AAACGAAAGGAGACTTATGAAATGTAATGAAACGAGAAAGACAGTA 782
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 143 -----PheLeuasnSerArgMetLeuMetProGlnaPrlleMetAlaTyr 157
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 783 ATATGTGTGTAGTTAGTTCTCCACACA-----TTAGGAGAA 818
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 158 ArgglYarggluValAlaGluAsnLeuProLeuargSerAlaProGly----- 174
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 819 AAAAGTATGTATGTGAAGATGTGGCAAGCCTTTAAAGCCTTCCAGCTTATTAATC 878
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 175 CysgluSerargAlaPheAlaProSerLeuTyrSerGlyLeuSerThrProPro----- 192
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 879 ATCAGAGATACATACAGAGAAACCTTACAAATGAAATGAGTGTGGCAAGCCTTTC 938
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 193 -----AlaserTyrSerMetTyr-----SerHsleuPro 202
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 939 ATCGGCGCTCACTTAAGTGTACCAAGGATGTCCATACAAAGAGAAATCATATCATAT 998
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

TYPE: DNA
ORGANISM: Rattus norvegicus
US-11-136-527-2436

Alignment Scores:

Pred. No.:	6,596-22	Length:	1578
Score:	472.50	Matches:	143
Percent Similarity:	39.8%	Conservative:	53
Best Local Similarity:	29.1%	Mismatches:	199
Query Match:	12.5%	Indels:	98
		Gaps:	16

US-10-755-889-18 (1-706) x US-11-136-527-2436 (1-1578)

```

QY 197 MetYSerHisLeuProValSerSerLeuLeuPheSerApsGluGluPheArgAerVal 216
DB 349 ATGTGGAAAGCTTACAGCCGAGCTGAGAGCTTCTGATGATGA----- 393
QY 217 ArgMetProValAlaAsnProPheProLyGluArgAlaLeuProCyAspSerAlaArg 236
DB 394 -----CCTGATCCTGAGAGAAAGTTATGATGATGATGATGATGATG 435
QY 237 ProValProGluLySerArgProThrLeuGluValSerProAsnValCyHisSer 256
DB 436 AAAAC-----TTAGCCTAGAACACACTTGTGACATAGAAAGAAACGCGGT 486
QY 257 AsnIleTySerProLySerGluThrIleProGluGluAlaArgSerApsMetHisTySer 276
DB 487 GGG-----GAAAGTCACCGGAGTGTAACCGAGTGTGTGAAGATTCTCG 531
QY 277 ValAlaGluLyLeuLyProAlaAlaProSerAlaArgAsnAlaProTyRheProCyAs 296
DB 532 AAGGCTCTTACCTTACTGACATCTGAGAAAGTCGCTACGAGGAGGAAATCATATGATGT 591
QY 297 AspLyAlaSerLySerGluGluGluArg-ProSerSerGluApsGluLeuAlaLeuHisP 316
DB 592 GGTACTGTGG-----AGAACCTTACGAGAGAGAGAACTTCC-----TT 633
QY 316 eGluProAsnAlaProLeuAsnArgLyGlyLeuValSerProGlnSerProGlnTy 336
DB 634 TCTCACCAGAAACACAGCTGTAAGAG-----GACCAGTGTGCTAGAGAA 681
QY 336 s-----SerApsCyGlnProAsnSerProThrGluAlaCySerSerLyAsnAlaCy 354
DB 682 ACCTCCGCTCCCATGACACACATCATGAGAAATCAGAGAAACGCGGAATTAACCATAT 741
QY 354 sIleLeuGlnAlaSerLySerProProAlaLySerProThrApsProLyAlaCyAs 374
DB 742 GCGGTAGAGAGTGTGGAAAGCT----- 766
QY 374 nTPrLyLyLeTyRlyPheIleValLeuAsnSerLeuAsnGlnAsnAlaLySProGly 394
DB 767 -----TTAATGGCAATCATATCTCAAGAAACATGAGAAATTCAT 807
QY 394 YProGluGlnAlaGluLeuGlyArgLeuSerProArgAlaTyThrAlaProAlaCy 414
DB 808 ACCGAGAGAAACCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 855
QY 414 sGlnProPheMetGlnProGluAsnLeuApsLeuGlnSer-----ProThrLySle 431
DB 856 CAGAGAGAGTACCTCATTT-AAACACAGAACGTCACAGTGGAGAGAGAGCTTTTAAGTG 914
QY 431 uSerAlaSerGlyLysPheSerThrIleProGlnAlaSerArgLeuAsnAlaLeu-- 450
DB 915 TAAATGAGTGTGTGAG-----GCTTTTACGAGAAAGAAACCTCATTTAT 959
QY 451 -----AsnArgSerMetThrGlySerProArgSerSerSerGluSerHisSerProLeuTy 469
DB 960 ACACGAGAGATCATACCGGAGAG----- 984
QY 469 rMetHisProProLySerCySerHisSerCyGlySerGlnSerProGlnHisAlaGluMetCy 489
DB 985 -----AAGCCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1040

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QY 489 sLeuHisThrAlaGlyProThrPheAlaGluGluMetGlyGluThrGlnSerGluTySe 509
DB 1041 CAGACACAGAGAGAGCCATCAT-----GGAGAGAA----- 1071
QY 509 rApsSerSerCyGlyAsnGlyAlaPhePheCyAsnGluCyAsnProCyAsrPheSerG 529
DB 1072 -----CCGTACACATGTAAGAAATTTGGGAAAGCTTACGCGG 1109
QY 529 uGluAlaSerLeuLyArgHisIleThrLeuGlnThrHisSerApsLyProTyRlyCyAs 549
DB 1110 CAATCAAAACCTGACGATGACATGAGAAATTCATATTTGAGAGAAACCTTATTAATGTA 1169
QY 549 pArgCyGlnAlaSerPheArgTyRlyGlyAsnLeuAlaSerHisLySerThrValHisP 569
DB 1170 CGAGTGTGAGAACATTTCTCAGCAGAGAGAGATCTCATCAACATCACACATTCACAC 1229
QY 569 rGlyGlyLySerProTyRArgCyAsnIleCyGlyAlaGlnPheAsnArgProAlaAsnLe 589
DB 1230 GAGCAGAGAGCCATGATGAGTGCATTAAGTCGAGAAAGCCTTTCTCGAATCACGTCGCT 1289
QY 589 uLySerHisIleThrArgIleHisSerGlyGluLySerProTyRlyCyGlyThrCyGlyAl 609
DB 1290 TATTTGCAATGAGAAATTCACACAGGCGATTAAGCCTTATGATGATGATGATGATG 1349
QY 609 aArgPheValGlnValAlaHisLeuArgAlaHisValLeuIleHisThrGlyGlySerP 629
DB 1350 AGCCTTCTGTCAGAGTCTCTCTTCAACCGTGCATGAGAGAGCCACACGCGTGAAGAAC 1409
QY 629 cTyRProCyGlyIleCyGlyThrArgPheArgHisLeuGlnThrLeuLySerHisP 649
DB 1410 GTATGCTCAATGAGTGTGAGAGCCTTTTCTCAGTTCTCAGCTTCTGCTTACAT 1469
QY 649 uArgIleHisThrGlyGlyLySerProTyRHisCyGlyLySerCyAsnLeuHisIlePheArg 669
DB 1470 GAGAAATCACACCTGAGGAGAGCCTTATCAGTGCAGTGAAGTGTGGAGAGCCTTACGCA 1529
QY 669 sLySerGlnLeuArgLeuHisLeuArgGlnLyS 680
DB 1530 GAAGTCCCAT-----CACATCAGACACAG 1554

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RESULT 7

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US-11-072-512-1778
; Sequence 1778, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHITO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: YOSHIMIZU, MOTOKI
; APPLICANT: NAGAHARA, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 08435-0191
; CURRENT APPLICATION NUMBER: US/11/072, 512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350, 978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096

```

Pred. No.: 1,16e-21 Length: 3090
 Score: 473.00 Matches: 165
 Percent Similarity: 40.0% Conservative: 68
 Best Local Similarity: 28.4% Mismatches: 200
 Query Match: 12.5% Indels: 150
 DB: 9 Gaps: 28

US-10-755-889-18 (1-706) X US-11-072-512-191 (1-3090)

QY 182 ProSerLeuTySerGlyLeuSerThrProProAlaSerTySerMetTySerHisLeu 201
 DB 519 CCATCGATG---TCMAATATCCACACCTGGCCTGAT----- 554
 QY 202 ProValSerSerLeuPheSerAspGluGluPheArgAspValArgMetProValAla 221
 DB 555 -----GATTCCTCTGCTCTTCA-----GAGTTTGG-CAATAGAAATGAAAAATACG 601
 QY 222 AsnProPheProLySGluArgAlaLeuProCyAsnAspSerAlaArgProValProGlyGlu 241
 DB 602 ACTCGGAATTTCTCTGAGAGAGAGATACCTGTGATGTA-----GAA 643
 QY 242 TyrSerArgProThrLeuGluValSerProAsnValCyHisSerAsnIleTySerPro 261
 DB 644 GTGGAAAGATTCAACAGGGAAGTTCCC-----TGCTGTCCAGTTTAGGTGATGCT 694
 QY 262 LysGluThrIleProGluGluAlaArgSerAspMetIleTySerValAlaGluGlyLeu 281
 DB 695 TGGGACTGT-----GAAACACAGAGGAGACACTTGAGGCACCTTAACTCTGGAG 748
 QY 282 LysProAlaAlaProSerAlaArgAsnAlaProTyRheProCyAspLyAspAlaSerLys 301
 DB 749 AAACCAAGGACTCAGGAAGCA-----ATTGTGAATATCCGTGTTT 790
 QY 302 GluGluGluArgProSerSerGluAspGluIleAlaLeuHisPheGluProProAsnAla 321
 DB 791 GGGAGACTTTGATTGGCAAGCTCAGAC-----CTTCCACCTCTCAGAGCA 835
 QY 322 ProLeuAsnArgLySGlyLeuValSerProGlnSerProGlnLysSer---AspGlyGln 340
 DB 836 GTTCTGGCAACAAATGGTTTCCATGCACTGCACTCAATGTTAGTGGTGGATGTGAC 895
 QY 341 ProAsnSerProThr-----GluAlaCySerSerLysAsnAla 353
 DB 896 CCCGCTTACCAGCTATCTTAAAGTTATGCAGATTAAGAACTCGGAGACAGTGAATGCC 955
 QY 354 Cys-----IleLeuGlnAlaSerGly-----Ser 361
 DB 956 TGTGGAAGAAAGCTCAACCATTCATGGAAGTTATTCATGGAAGAAATCCAGTGAAGAG 1015
 QY 362 ProProAlaLySerProThrAspProLyAspAlaCyAsnTrp----- 375
 DB 1016 AAGCCCTTACAAATACCTCGAAAGTGTAACTTTTATCATTTTAACTCTCTTGTCAT 1075
 QY 376 -----LysIleTyRlys-----Phe 380
 DB 1076 CAGAAATTAATGAAGAGCGCAAGAAATCGTATGAAGTAAAGATTGGAACACTCTTT 1135
 QY 381 IleValLeuAsnSerLeuAsnGlnAlaAsnAlaLys-----ProGlyGlyProGluGln--- 397
 DB 1136 ACTCGAGCTCATGCTTAATGAAGAAACAGAGAAATCTCCGTGAGAGAAACAAATATAGA 1195
 QY 398 ---AlaGluLeuGlyArg-----LeuSerProArgAla 407
 DB 1196 TGTACTGATGTGGCAATGCTTCAACAGCACTCTCTCTGTGTTTTCATCAACGAACT 1255
 QY 408 TyrThrAla-----ProProAlaCyGlnPro-----PrometGluProGluAsnLeu 423
 DB 1256 CACACCGAGAGAGAGCCTTATATCTTGTATAGTGTGAAAGTCTCTTCCACAGCACTAC 1315
 QY 424 AspLeu-----GlnSerProThrLysLeuSerAlaSer 434
 DB 1316 AACCTGATTGTGCATCAAGATCCACACAGGAGAGAGCCCTTATGAATGCATGAATGT 1375

QY 435 Gly-----GluAspSerThrIleProGlnAlaSerTyRlysLeuAsnIleVal 450
 DB 1376 GGGAAAGCTTTCAGTATGGCTCAGCTCGACACACACAGCAGAAATTCAC----- 1426
 QY 451 AsnArgSerMetThrGlySerProArgSerSerSerGlnSerHisSerProLeuTyRMet 470
 DB 1427 -----ACAGCCGAG----- 1435
 QY 471 HisProProLySGlySerSerCyGlySerGlnSerProGlnHisAlaGluMetCyLeu 490
 DB 1436 AAACCTTATGAATGCCATGAGTGTGAAAAACCTTCAACGAAATTCATCTTAATTTTG 1495
 QY 491 HisThrAlaGlyProThrPheAlaGluGluMetGlyGluThrGlnSerGluTyRSerAsp 510
 DB 1496 CACCAAGAACTATACA-----GGGGAAGAA----- 1522
 QY 511 SerSerCyGluAsnGlyAlaPhePheCyAsnGlnCyAspCyAsnArgPheSerGluGlu 530
 DB 1523 -----CCATATAGATGTACGAATGTGGAAACCTTCACTGACATC 1564
 QY 531 AlaSerLeuLysArgHisThrLeuGlnThrHisSer---AspLysProTyRlysCyAsp 549
 DB 1565 TCCACCTTACAGTGCAAT---CTCAGAAATCCACACCGGTGAGAAAGCCTTATGATGTAGC 1621
 QY 550 ArgCyGlnAlaSerPheArgTyRlysGlyAsnLeuAlaSerHisLysThrValHisThr 569
 DB 1622 AAATGTGAAAGGCTTTCCGGAGCGGCTCGTACTCCACAGCATGAGAGACTCACACT 1681
 QY 570 GlyGluLysProTyRArgCyAsnIleCyGlyAlaGlnPheAsnArgProAlaAsnLeu 589
 DB 1682 GGAGAAAGCCCTTGTAGTGTGACAGAGTGGGGAATCTTCAACAGAAATCTCACCTC 1741
 QY 590 LysThrHisThrArgIleHisSerGlyGlyLysProTyRlysCyGluThrCyGlyAla 609
 DB 1742 ATTGTGCATCAAAAGATTCATTTCTGGAGAAACCTTATGAATGAAGATGTGGCAAG 1801
 QY 610 ArgPheValGlnValAlaHisLeuArgAlaHisValLeuIleHisThrGlyLysPro 629
 DB 1802 ACTTTCATCGAGAGTGGTCACTCATCAGGACATCAGAGATTCATCTGCGAGAAAGCCC 1861
 QY 630 TyrProCyGluLysLeuGlyThrArgPheArgHisLeuGlnThrLeuLysSerHisLeu 649
 DB 1862 TATGCTGCAACCAAGTGTCAAGAACTTTTCAAGAAATTCCTGCGCTCATTAAGCACAG 1921
 QY 650 ArgIleHisThrGlyGlyLysProTyRHisCyGlyLysCyAsnLeuHisPheArgHis 669
 DB 1922 AGCATCATCTGTGTGAAAGCCCTTATGAGTGTATCAGTGTGCAAAAGCCTTCAAGGAC 1981
 QY 670 LysSerGlnLeu-----ArgLeuHis-LeuArgGlnLysHisGlyAlaIleThr 685
 DB 1982 AGCTCTGTCTGACCAAGCAGCAGAGAAATTCACCTAAAGAGAGCCCATATCAGTGTCCA 2041
 QY 685 rAsn 686
 DB 2042 GAAT 2045

RESULT 6
 US-11-136-527-2436
 ; Sequence 2436, Application US/11136527
 ; Publication No. US20050287570A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
 ; FILE REFERENCE: 031896-041000 (AM101086)
 ; CURRENT APPLICATION NUMBER: US/11/136,527
 ; CURRENT FILING DATE: 2005-05-25
 ; PRIOR APPLICATION NUMBER: US 60/574,294
 ; PRIOR FILING DATE: 2005-05-26
 ; NUMBER OF SEQ ID NOS: 362830
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 2436
 ; LENGTH: 1578

```

Db      1002 ----GCTGTGTTGTTTCAACCCAGAGAAATGGTGTGTTTCTGACTCTACTCAGAGAGCCT 1057
Qy      213 -PheArgPValArgMet-----ProValAlaAsnProPheR 225
Db      1058 GATATAGATGTGATGCTGTGAGAACTACAGAACTGGCTGTGTGGCTGATCACTGG 1117
Qy      225 oLysGluArgAlaLeuProCysAspSerAlaArgProValProGlyGluTyrSerArgP 245
Db      1118 CAATCCCAATGGCTGTCTTATTTTGAGAAAGA-----GGAGACAGTGCACAC 1168
Qy      245 oThrLeuGluValSerProAsnValCysHisSerAsnIleTyrSerProGlyGluThrI 265
Db      1169 TCACAGAGGGGCTCTCTCAGACACCTGTGCAGAACTCAGTGTCAACCCCAAGAGCAAT 1228
Qy      265 eProGluAlaArgSerAspMetHisTyrSerVal---AlaGluGlyLeuLysProAl 284
Db      1229 TCCTAGCCCAAGATCTTTACAGAGATCCTGTCTCATGTGATGTGAAGGGAGCAACT-- 1286
Qy      284 aAlaProSerAlaArgAsnAlaProTyrPheProCysAspGlyAlaSerLysGluGlu 304
Db      1287 -CAGCTTGAGAGAAACTCTATATATATATGAACTTGAGAACTTTTAAACAGCATTA 1345
Qy      304 u-ArgProSerSerGluAspGluIleAlaLeuHisPheGluProProAsnAlaProLeu 324
Db      1346 ACCACTTTTCCAGTACCAAGAAATTCATGCTGAG-----AGGCATCTGTGA 1393
Qy      324 sNArgLysGlyLeuValSerProGlnSerProGlnLysSerAspCysGlnProAsnSerP 344
Db      1394 ATCTCAAGAGATTAGAAATTCCTCTTCC-----AGAGTGC 1429
Qy      344 rOThrGluAlaCysSerSerLysAsnAlaCysIleLeuGlnAlaSerGlySerProPro 364
Db      1430 CCACCTAATGTGTC-----CCGA 1447
Qy      364 lAlaSerSerProThrAspProLysAlaCysAsnTrpLysTyrLysPheIleValLeu 384
Db      1448 GAAATATCC-----GTAGTGGGAGATTA 1468
Qy      384 sNserLeuAsnGlnAsnAlaLysProGlyGlyProGluGlnAlaGluLeuArgLeu 404
Db      1469 AT----- 1470
Qy      404 ePProArgAlaTyrThrAlaProProAlaCysGlnProPoweGluProGluAsnLeu 424
Db      1471 -----CCTATGCATGTAACAATGTGA 1492
Qy      424 sPLeuGlnSerProThrLysLeuSerAlaSerGlyGluAspSerThrIleProGlnAla 444
Db      1493 AAAATCTTCATGATACAGCTGTGACCTTATCAGGCACTGAGAGAACTCATCTCAGAGAA 1552
Qy      444 eArgLeu-----AsnAsnIleValAsnArgSerMetThrGlySerProArgSerSer 462
Db      1553 GTGCTTTGACTGTCAAGAAATGTGGCAAGCTTCA-----AATATTCCTCGAATCTCCG 1606
Qy      462 eArgLysHisSerProLeuTyrMetHisProPro---LysCysThrSerCysGlySerG 481
Db      1607 GCGACACATGAGAAACCATAC--GAGAGAGAACCATTTGATGTAGTCACTGTGTGGAGAAA 1665
Qy      481 InSerProGlnHisAlaGluMetCysLeuHisThrAlaGlyProThrPheAlaGluGlu 501
Db      1666 CTTTCAGAGAACTTTAACTGATTTTGCACAGAGAAACACACA----- 1712
Qy      501 eGlyGluThrGlnSerGluTyrSerAsp-----SerSer 513
Db      1713 --GAGAGAGAGCCCTACAGATGTAAAGATTGTGGAAAGCCTTCAATCAGCANTCACC 1770
Qy      513 yGluLysGlyAla-----PhePheCysAsnGluCysAspC 525
Db      1771 TCAGAGACCACTGTAGAACTCACACTGAGAGAGAACCTTTGATGTAGCAGCAGTGTGGA 1830
Qy      525 yArgPheSerGluGluAlaSerLeuLysArgHisThrLeuGlnThrHisSer---Asp 544
Db      1831 AAGCTTTCAGAGAACTTTCATCTTCAAGACACAT--CTGCAAACTCATACAGAGAGA 1887

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Qy      544 yPProTyrLysCysAspArgCysGlnAlaSerPheArgTyrLysGlyAsnLeuAlaSerH 564
Db      1888 AACCATATGATATGCAACAGATGTGGCAAGCCCTTCCGACAGACATCATCTGAACGTGC 1947
Qy      564 lAlaThrValHisThrGlyGluLysProTyrArgCysAsnIleCysGlyAlaGlnPhe 584
Db      1948 ACAAGAGATACACAGAGGAGAACTGTATAGTGTGGCAGCTTGGCTCAGCTTCA 2007
Qy      584 sNArgProAlaAsnLeuLysThrHisThrAlaGlnHisSerGlyGluLysProTyrLysC 604
Db      2008 GTGCTCTTTCACACCTGAAGAGTGCATGCGAACTCACACTGAGAGAAAGCCCTATGTGT 2067
Qy      604 yGluThrCysGlyAlaArgPheValGlnValAlaHisLeuArgAlaHisValLeuIleH 624
Db      2068 GCCAGAAATGTGGGAGACCTTCAGTGTGAGCCCTCATCTCCAGAAACAGAGAGATC 2127
Qy      624 lThrGlyGluLysProTyrProCysGlyIleCysGlyThrArgPheArgHisLeuGlnT 644
Db      2128 ACAGTGGCAAGAGCCCTATGATGATCCAGAAATGGCGGAGCCCTTGTGCTGATTCAC 2187
Qy      644 hLeuLysSerHisLeuArgGlnHisThrGlyGluLysProTyrHisCysGlyLysCysA 664
Db      2188 ATCTTATGTATGATGATGAGAACACAGATGCGGAGAGCCCTATCATAGTATATCAGTGTG 2247
Qy      664 sNLeuHisPheArgHisLysSerGlnLeuArgLeuHisLeuArgGlnLysHisGlyAlaI 684
Db      2248 AGAAAGCCCTTCAGGACAGCTCTTCATCATCTGACAAAGAAACCACTGTGGAGAG 2307
Qy      684 lThr 685
Db      2308 AGACC 2312

RESULT 5
US-11-072-512-191
; Sequence 191, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOMYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: NASUDO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 08435-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 191
; LENGTH: 3090
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-072-512-191

Alignment Scores:

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Db      797 ATGTAAGTCGTGTGAGAAAAAACCCTTCACTTAACACTATCCCTTGTGAACATGAGAAAAA 856
Qy      392 ogylygylprogluIn-----
Db      857 CCATAGTGTGAGAGAAACCTATTATAGTGAAGAATGTTCAAAAGCCTTAGCCCAAGTTC 916
Qy      398 -----AlagluLe 400
Db      917 AGCTCTATTTCACATCAATTAACACATCTAGGAGAGAAACCCTACATATGTAAAGAAATG 976
Qy      400 uGlyArgLeuSerProArGAlaYrThrAlaProProAlaCyBgInProPoweGluPr 420
Db      977 TGGG-----AAAGCCTTACTCTCAGTACATCCCTTATTAAGCATTAAGAAC 1024
Qy      420 oGluAsnLeuAspLeu-----
Db      1025 CCATACCTGTGAGAAATCTTACAGATGTAAAGAAATGTGTAAATCCTTCAAGCCGAGATC 1084
Qy      426 -----GlnSerProThrArgLeuSer----- 432
Db      1085 AGGCTTTTATATACATCAAAATATTCATGCTGAAGAAACCCTGTATATATATCCGG 1144
Qy      433 -----AlaSerGlyGluAspSerThrIleProGlnAlaSerArgLeuAsnAlaIva 450
Db      1145 TAGGAAGGATCTAGTGTGACACATCCCTTTCGATGTGAAGAATCATCTTAGAAA 1204
Qy      450 lAsnArgSerMetThrGlySerProArgSerSerGlnSerIleSerProLeuYrme 470
Db      1205 GAAGTCTCTATTATGTATGAATGTGGCAACCTTAAAGCTTACATCCCTTCGTTA 1264
Qy      470 thIa-----ProProLysCyBhrSerCyBgInSerGlnSe 482
Db      1265 TCATCAAGAAATTCACACTGAGAGAAACCTTTTAAATGATGTAATGTGAGAGACCTT 1324
Qy      482 rProGlnHIsAlaGluMetCyBleuHIsThrAlaGlyProThrPhaAlaGluGluMetG 502
Db      1325 CAGCCAGAGTCCCTCTCTTATTCACAT-----GAAAGAAATTC 1363
Qy      502 yGluThrGlnSerGluYrSerAspSerSerCyBgInuAsnGly----- 516
Db      1364 CACCGAGAAAGCCCTATAGATGCAATGATGCGAAAGCCTTACTTCAATTCACG 1423
Qy      517 -----AlaPhePheCyAsnGluCyAs 524
Db      1424 ACTTAATAGACACCGAATCATTCATATCTGAGAGAAATATATATATATATATATATG 1483
Qy      524 pCyAsrPheSerGluGluAlaSerLeuLysArgHIsThrLeuGlnThrHIsSerAspLy 544
Db      1484 TAAAGCCTTAAGCTCCCACTCAACACTTATTAATTCACAGAGGAATTCATCTGAGAAA 1543
Qy      544 sProTyLysCyAspArgCyBgInAlaSerPheArgTyLysGluAsnLeuAlaSerHIs 564
Db      1544 ACCATGTAAATGTAAAGTATGTGAAAGCCCTTCAAGACAGATTCAAGCTTCATTCACA 1603
Qy      564 slySerThrValHIsThrGlyGluLysProTyArgCyAsnAlaIleCyBgInAlaGlnPheAs 584
Db      1604 TCAGAGAAATGCAATCTGAGAGAAAGCCCTATTAAGTAAACAGATGTGGGAAAAACATTAG 1663
Qy      584 nArgProAlaAsnLeuLysThrHIsThrArgTlHIsSerGlyGluLysProTyLysCy 604
Db      1664 GTGTAACTCATCATTAAGTAAATCACCAGAGAAATTAATCTGAGAGAAACCATATACATG 1723
Qy      604 sGluThrCyBgInAlaArgPheValGlnValAlaHIsLeuArgAlaHIsValLeuIleHIs 624
Db      1724 TGAGGAATCTGGGAATCTTTTGGGCAAGTTCAAGCTCTTATTCAGCATTCGAAGATTCA 1783
Qy      624 sThrGlyGluLysProTyArgProCyBgInuLleCyBgInYrThrArgPheArgHIsLeuGlnTh 644
Db      1784 TACAGAGAGAAAAACCTTTAAATGTAAATCAGTGTGAAAAACCTTTAGCAAAAGCTCATC 1843
Qy      644 rLeuLysSerHIsLeuArgTlHIsThrGlyGluLysProTyArgHIsCyBgInuLysCyAs 664

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Db      1844 ACCTATTCACATCAGAGAAATTCATATCTGAGAGAAACCTTATGAATGTAAATCATGTGG 1903
Qy      664 nLeuHIsPheArgHIsLysSerGlnLeuArgLeuHIsLeuArg 678
Db      1904 GAAACTTTTCAACCATATAGGTGATCCCTTACTATCATTTAA 1946

RESULT 4
US-11-072-512-1944
; Sequence 1944, Application US/11072512
; Publication No. US2006002945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: MAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUDKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: INIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072, 512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350, 978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1944
; LENGTH: 2784
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-072-512-1944

Alignment Scores:
Pred. No.: 8.39e-22 Length: 2784
Score: 474.50 Matches: 167
Percent Similarity: 39.6% Conservative: 72
Best Local Similarity: 27.7% Mismatches: 228
Query Match: 12.5% Indels: 137
Gaps: 21

US-10-755-889-18 (1-706) x US-11-072-512-1944 (1-2784)
Qy      130 AlagluMetValSerAlaIleLysProProArgGluGluPheLeuAsnSer-ArgMetLe 149
Db      776 GCCGCCCTGTGGCTCTGGGATGACGAGGACGAGGAGCCGCTATGCAAGTTCGAGAGGTGCT 835
Qy      149 uMetProGlnAspIleMetAlaYrArgGlyArgGluValAlaGluAsnAen---LeuPr 168
Db      836 GATACCACTGCTTACATCTGGGCCACCGCAACCCATGGGTGCGCAGGGATTCGTGCTGTGCC 895
Qy      168 cLeuArg-----SerAlaProGlyCyBgInSerArgAlaPheAlaProSe 183
Db      896 TGCAAGTGAACCTGCTGCTTCAAGAGGACAAAGTGAAGGAAGGATATGGCTCTGG 955
Qy      183 rLeuTySerGlyLeuSerThrProProAlaSerTySerMetTyrSerHIsLeuProVa 203
Db      956 GCTGCAACCGCCTGTTTACAGAAACCATGACCTTTGCAAGATGG----- 1001
Qy      203 lSerSerLeuAspSerAspGluGlu----- 212

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1413 AGGCTCCACAGGGCT----- 1427
1426 GlnSerProThrLysLeuSerAlaSerGlyGluApsSerThrLeuProGlnAlaSerArg 445
1428 GAGAACGCTTAATTAATGTAGAGAAATGTGTAAAGGCTTCACT-----CAGCTGACAT 1481
446 LeuAsnAsn1LeuAlaAsnArgSerMetThrGlySerProArgSerSerSerGlu----- 463
1482 TTT---CACATTCATCAGAGAGTCCACATGAGAGAAACCTTACAGTGTATGTGTGT 1538
464 -----SerLeu---SerProLysTyMetHis----- 471
1539 GGTAAAGGCTTCAGCCCAATTCACCAATTAATATGCCATCGAGAGTCCACAGAGAG 1598
472 ---ProProLysSerGlySerGlySerGlnSerProGlnHisAlaGluMetCysLeu 490
1599 AAGCCATACAGTGTAGAGCGGTGTGGAAAGGCTTACCCGTAAATACAGATCTGCATATT 1658
491 HisThrAlaGlyProThrPheAlaGluGluMetGlyGlyThrGlnSerGlyTySerAsp 510
1659 CAT-----TTCAAGTTTCAACGGAGAG-----AAACCTTAATATGT 1697
511 SerSerCysGluAsnGly----- 516
1698 AAGAGTGTGTAAAGGCTTCAAGTCAAGCTTCAATCTTCAAGTCCATCAGAAATGTCCAC 1757
517 -----AlaPhePheCysAsnGluCysAspCysArgPheSerGlnGluAlaSer 532
1758 ACTGGGAGAAACGATTCAATGTGAAAGCTGTGGAAAGGCTTCAAGTCTCACTCAAAAG 1817
533 LeuArgHisThrLeuGlnThrHisSerAspLysProGlyCysAspArgCysGln 552
1818 CTTCAAAACCATCAGAGAGTCCACATCGAGAGAAACCAATATAGATGTATGTGTGTGT 1877
553 AlaSerPheArgTyLysGlyAsnLeuAlaSerHisLysThrValHisThrGlyGlyLys 572
1878 AAGCATTCAGATTATGTTCAATCTTAACTCAACAGTAATTCACACTGGAGAAAAA 1937
573 ProTyArgCysAsn1LeuGlyAlaGlnPheAsnArgProAlaAsnLeuLysThrHis 592
1938 CCAATAAATGTAGAGAAATGTGGAAAGGCTTCAAGTGTGAGATCAAAATCTTCAAGCAT 1997
593 ThrArg1LeHisSerGlyGlyLysProGlyCysGlyLysCysGlyAlaArgPheVal 612
1998 CAAGAGTTCACACAGAGAAAAAACCTTAATATGTAGAGAGTGTGTAAAGCTTCAAT 2057
613 GlnValAlaHisLeuArgAlaHisValLeu1LeHisThrGlyGlyLysProGlyProCys 632
2058 CAGGCCATAGATTTCGGGTATCATCAGAGAGTCCATATCTGAGAGAGCCATCAAAATGT 2117
633 Gln1LeuGlyLysThrArgPheArgHisLeuGlnThrLeuLysSerHisLeuArg1LeHis 652
2118 GGTGTCTGTGTAAAGGCTTCAAGTCAAGTCTGTGTCTTCAATCCATCAGAGAGTCCAC 2177
653 ThrGlyGlyLysProGlyCysGlyLysCysAsnLeuHisPheArgHisLysSerGln 672
2178 ACGGGGAAAAAGCATTAATATGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2237
673 LeuArgLeuHisLeuArgGlnLysHisGly 682
2238 TTTATATACCATCAGAGAGGCCACACTGA 2267

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RESULT 3
US-11-000-688-1136
; Sequence 1136, Application US/11000688
; Publication No. US2005028754A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, Francois
; APPLICANT: HOUJATTE, Remi
; APPLICANT: BIRNBAUM, Daniel
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
; FILE REFERENCE: 1423-R-03

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; CURRENT APPLICATION NUMBER: US/11/000,688
; CURRENT FILING DATE: 2004-12-01
; PRIOR APPLICATION NUMBER: US 60/525,987
; PRIOR FILING DATE: 2003-12-01
; NUMBER OF SEQ ID NOS: 1596
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1136
; LENGTH: 2435
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial sequences: primer
; NAME/KEY: misc_feature
; LOCATION: (1)..(2435)
; OTHER INFORMATION: zinc finger protein 354a(ZNF354A) gene..
US-11-000-688-1136

Alignment Scores:
Pred. No.: 6,84e-22 Length: 2435
Score: 475.00 Matches: 152
Percent Similarity: 38.0% Conservative: 82
Best Local Similarity: 24.7% Mismatches: 205
Query Match: 12.5% Indels: 177
DB: Gaps: 16

US-10-755-889-18 (1-706) x US-11-000-688-1136 (1-2435)

205 SerLeuLeuPheSerAspGluGlu-----Phe 213
210 GCTGTGCTGTTTACCGAGATAGTGAGAAAGCTGCCCTTTCAGAGAACTTGTAC 269
214 ArgAspValArgMet-----ProValAlaAsnProPheProlys 226
270 CCGGATGTGATGCTGTGAGAACTATAGAACTGTCTCACTGAGGCTCCCATTTACCAA 329
227 GlnArgAlaLeu-ProGlyAspSerAlaArgProVal-ProGlyGlyLysTySerArgProth 246
330 CCAAAAGTATCTCCTGTTGCGAGAGAGAAAGATCCCTGTGAGGTGAGAAAGCGGT 389
246 rLeuGluValSerProAsnValCysHisSerAsn1LeuTySerProLysGlyThrLepr 266
390 TCTGGC-GTCTCCTCTCTAGATCGAAGAGCGTATAAACCAAAATCAACGCAAC 448
266 oGluGluAlaArgSerAspMetHisTySerValAlaGluGlyLeuLysProAla1a1aDr 286
449 ACAAGAC-----TCTCATTTCAAGGACTG---ATACTGAAGAAG 484
286 oSerAlaArgAla1aProTyL----- 293
485 ATCCAAACAGAAATGATACCTTGGATTGAAATTAAGAAAGCCTTACATATATGAAGCGAG 544
294 -----PheProCysAspLysAlaSerLysGluGln 303
545 ATTAGAGAAAAACGAGATTAAGAAAGGAAAGTTTTCAGATATGTTTCCAGCCACCAAAAA 604
303 u-----GluArgProSerSerGlyLysArgGlu1LeuAlaLeuHisPheGluProPr 319
605 AATCCCACTTAATAGAAAGAACCATTAATAATCTGAATGTAGAGCAAAATTCAGCCCAA 664
319 oAsn1aProLeuAsnArgLysGlyLeuValSerProGlnSerProGlnLysSerArgCys 339
665 GTCAAGTCTTAATTAAGCAACAGATATCTTCCAGAGAAAGAAACCAACCAAAATGTAAAT 724
339 eGlnProAsnSerProThrGluAlaCysSerSerLysAsnAlaCys1LeuGlnAlaSe 359
725 ACAAGAAACAGC-----CTCAACAGATTTCAATTTCTT----- 761
359 rGlySerProAlaLysSerProThrAspProLysAlaCysAsnTrpLysLysTyLys 379
762 -----AATCAACCAAAATTAACGACAGATTAACGCTATATA 796
379 s-----Phe1LeuAlaLeuAsnSerLeuAsnGlnAlaAsn1aLysPr 392

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Qy 701 GlutProlyserAlaCys 706
 Db 2428 GAGCTCCCAAGCTTC 2445

RESULT 2

US-11-072-512-959
 ; Sequence 959, Application US/11072512
 ; Publication No. US200602945A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ISOGAI, TAKAO
 ; APPLICANT: SUGIYAMA, TOMOYASU
 ; APPLICANT: OTSUKI, TETSUJI
 ; APPLICANT: MAKAMATSU, AI
 ; APPLICANT: SATO, HIROYUKI
 ; APPLICANT: ISHII, SHIZUKO
 ; APPLICANT: YAMAMOTO, JUN-ICHI
 ; APPLICANT: ISONO, YUDKO
 ; APPLICANT: HIO, YURI
 ; APPLICANT: OTSUKA, KAORU
 ; APPLICANT: NAGAI, KEIICHI
 ; APPLICANT: IRIE, RYOTARO
 ; APPLICANT: TAMECHIKA, YCHIRO
 ; APPLICANT: SEKI, NAOHICO
 ; APPLICANT: YOSHIKAWA, TSUTOMU
 ; APPLICANT: OTSUKA, MOTOKUKI
 ; APPLICANT: NAGAHARI, KENJI
 ; APPLICANT: MASUHO, YASUHIKO
 ; TITLE OF INVENTION: Novel full length cDNA
 ; FILE REFERENCE: 084335-0191
 ; CURRENT APPLICATION NUMBER: US/11/072,512
 ; CURRENT FILING DATE: 2005-03-07
 ; PRIOR APPLICATION NUMBER: US 60/350,978
 ; PRIOR FILING DATE: 2002-01-25
 ; PRIOR APPLICATION NUMBER: JP 2001-379298
 ; NUMBER OF SEQ ID NOS: 4096
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 959
 ; LENGTH: 3052
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-11-072-512-959

Alignment Scores:
 Pred. No.: 1,23e-23 Length: 3052
 Score: 503.00 Matches: 190
 Percent Similarity: 35.5% Conservative: 83
 Best Local Similarity: 24.7% Mismatches: 265
 Query Match: 13.3% Indels: 232
 DB: 9 Gaps: 34

US-10-755-889-18 (1-706) x US-11-072-512-959 (1-3052)

Qy 33 AspValValIleValIleValSerArgIUGInPheArgAlaHisIleYThrValIleuMetAla 52
 Db 294 GATTTGGCTGTGCTTCTTCCAGGAGGAAGACTGCGA-----CTGCTGATCTTACC 344
 Qy 53 CysSerGlyLeuPheTySerIlePheThrAspGlnLeuIleCysAsnLeuSerValIle 72
 Db 345 CAGAGGAAGCTGTACCGAGATGTCATGTGTGAGAACTTCAAG---AACCTGTTGCAAGTG 401
 Qy 73 AsnLeuAspProGluIleAsnProGluIlePheCysIleLeuLeuAspPheMetCysThr 92
 Db 402 GGGCATCTTCCC---TTCCAAACCAAGAT-----ATGGTA 431
 Qy 93 SerArgLeuAsnLeuArgIUGIleValMetAlaValMetAlaThrAlaMetCysIleu 112
 Db 432 TCCCAATTTGGAAGCAAGAAAGAAAGCTTTGATGATGAGAAACAGAAACCCAAAGAGAGCG 491
 Qy 113 GlnMetGluHisValIleAspThrCysArgIlePhe----- 124
 Db 492 AAGCATCAAAATTAAGATGAGAAACACTCCAAAAATTTGATTAAATATACCTTTCAATCA 551

Qy 124 ----- 124
 Db 552 GAGCTGCTGTGCGAAATCTGAAACAGTTGCAAGTGAATTAACAGTCTCTTACG 611
 Qy 125 -----IleValAsnGluIleGluMet--- 132
 Db 612 GGGAAAGTTCCAGTTATTATTAAGGTACTATTATTCAGTTCTGAAAATGGAACAAT 671
 Qy 133 -----ValSerAlaIleYAspProArgIUGIlePhe----- 143
 Db 672 ATTAATGACCTTAAGAGATAGTACTATTATTAATGAAAATGCAAGGTTCCATTTTGG 731
 Qy 144 -----LeuAsnSerArgMetLeuMetProGlnAspIleMetAlaTyArg 158
 Db 732 AGAACCCAGCATCTTCCGGGAATATATATCTAGTACAGATTCAGAGT---AGA 788
 Qy 159 GLYArgGluVal---ValGluAsnAsnLeuPro-----LeuArgSerAla 172
 Db 789 GGTAAAGCAATTATGTAATAATTAACCTGCAATATCATGAGACTTCATGAAGAAATCA 848
 Qy 173 ProGlyCysGluSerArgAlaPheAlaProSerIleuTySerGlyLeuSerThrProPro 192
 Db 849 CCA-----TTTCATGACATATTAAACTGACACAGAACCAAAACC 890
 Qy 193 AlaSerTySerMetTySerHisLeuProValSerSerIleuPheSerAspGluIle 212
 Db 891 TGCAAAGTAAATGATATGCAAA-----ATCATTAATGATGGCTCC 932
 Qy 213 PheArgAspValArgMetProValAlaAsnProPheProIleGluArgAlaLeuProCys 232
 Db 933 -----AACCAAGAAATTAACCTTAAGA-----GAGAAACCCCATCTCATGT 971
 Qy 233 AspSerAlaArgProValProGlyGluTySerArg-----ProThrLeu 247
 Db 972 -----GTTGACTGTGAAAGGGCTTCACTTATAGCCCAAGCTT 1010
 Qy 248 GluValSerProAsnVal-----Cys-----HisSerAsnIleTy 259
 Db 1011 CCCCTTATCCGATGATTTTCAACAGAGAAAATGCTTCACTGACAAAGCTCATCTCGA 1070
 Qy 260 SerProIleGluThrIleProGluGluAlaArgSerAspMetHisTySerValAlaGlu 279
 Db 1071 ACTCATCAGAGAAATTCACCCAGAGAGAAATCAATGATGATGATGATGATGCTGATTGC 1130
 Qy 280 GlyLeuAspProAlaAlaProSerAlaArgAsn-----AlaProTyPhePro 295
 Db 1131 TTCAATTAAGAGCTCTTTTCAATTTCTTATCAATCTATATCATACAGAGAGAACTTATAGA 1190
 Qy 296 CysAspIleValAsnIleGluGluIleArgProSerSerGluAspGluIleAlaLeuHis 315
 Db 1191 TGGGACAGTTGGCGGCAAGGATTC-----AGTAGCAGACAGGGCTTATCATTCAT 1241
 Qy 316 PheGluProProAsnAlaProLeuAsnArgIleValSerProGlnSerProGln 335
 Db 1242 TACGAACTCATACTGGA-----GAGAAACCTTAT 1271
 Qy 336 IysSerAspCysGlnProAsnSerProThrGluAlaCysSerSerIleAsnAlaCysIle 355
 Db 1272 AAA-----TCCAGAGAAATGTGAAATGCTTT 1298
 Qy 356 LeuGlnAlaSerGly-----SerProProAlaIle 365
 Db 1299 AGTCAAGATTCAATTTTCACTGATGATCAGAGATCACTGAAAGAAACCAATACAA 1358
 Qy 366 SerProThrAspProIleValCysAsnTrpIleValSerIleValLeuAsnSer 385
 Db 1359 TGCAGAGAGTGTGTAAGGCTTGGCTTGG-----AGT 1391
 Qy 386 LeuAsnGlnAsnAlaIleProGlyGlyProGluGlnAlaGluLeuGlyArgLeuSerPro 405
 Db 1392 GTTATCTC-----CGTGTTCACAG 1412
 Qy 406 ArgAlaTyThrAlaProProAlaCysGluProProMetGluProGluAsnLeuAspLeu 425

Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 12 Gaps: 0
 US-10-755-889-18 (1-706) x US-11-122-329-70 (1-3536)

QY 1 MetAlaSerProAlaSerCyAlIeGlnPheThrArgHisAlaSerAspValLeuLeu 20
 DB ATGGCTCCGCGGCTGACAGCTGTATCCAGTTCACCCGCCATGCCAGTGTCTTCTTC 387
 QY 21 AsnLeuAsnArgLeuArgSerArgAspIleLeuThrAspValValIleValValSerArg 40
 DB AACCTTAATGCTCTCGAGTCAACATCTTGAAGTGTGTCAATGTGTGACCCGT 447
 QY 41 GluGlnPheArgHisIleValThrValIleuMetAlaCysSerGlyLeuPheTyrSerIle 60
 DB GAGCACTTTAGACCCCATTAACGATCTTCATGCGCTGACGTGGCTGTTCTATACATC 507
 QY 61 PheThrAspGlnLeuLysCysAsnLeuSerValIleAsnLeuAspProGluIleAsnPro 80
 DB TTTACAGACACAGTGAATGCAACTTATGTATCAATCTAGATCTTGAATCAACCT 567
 QY 81 GluGlyPheCysIleLeuLeuAspPheMetTyrThrSerArgLeuAsnLeuArgGluGly 100
 DB GAGGAGTTCGACATCTCTGACCTTCAATGATACATCTTGCCTCAATTTGGCGAGGCG 627
 QY 101 AsnIleMetAlaValMetAlaThrAlaMetTyrLeuGlnMetGluHisValIleAspThr 120
 DB 628 AACATCATGGCTGTGATGGCCACGCTATGTACTGCAATGAGCATGTGTGACACT 687
 QY 121 CysArgLeuPheIleValAlaSerGluValGluMetValSerAlaIleLysProProArg 140
 DB 688 TGCCTGAAAGTTTATTAAGCCAGTGAAGAGATGTTTCTGCCATCAAGCTCTCTCGT 747
 QY 141 GluGlnPheLeuAsnSerArgMetLeuMetProGluAspIleMetAlaTyrArgGluArg 160
 DB 748 GAAGAGTTCCTCAACAGCCGAGATGCTGATGCCCAAGACATCAATGCTTACGAGGCT 807
 QY 161 GluValValGluAsnAsnLeuProLeuArgSerAlaProGlyCysGluSerArgAlaIle 180
 DB 808 GAGGTGTGAGAAACAACCTGCCACTGAGAGAGCGCCCTGGGTGAGACAGACCTTT 867
 QY 181 AlaProSerLeuTyrSerGlyLeuSerThrProProAlaSerTyrSerMetTyrSerHis 200
 DB 868 GCCCCAGCCTGTACAGTGGCTGTCCACACGCCAGCCTCTTATTCAGTACAGCAC 927
 QY 201 LeuProValSerSerLeuLeuPheSerArgGluGlnPheArgAspValArgMetProVal 220
 DB 928 CTCCTGTGACAGCCTCTCTTCTCGATGAGAGATTGCGGATGTCCGATGCCCTGTG 987
 QY 221 AlaAsnProPheProLysGluArgAlaLeuProCysAspSerAlaArgProValProGly 240
 DB 988 GCCAACCTTCCCTCCAGAGAGCGGCGACCTCCATGTATGTGCCAGCGCAAGTCCCTGT 1047
 QY 241 GluTyrSerArgProThrLeuGluValSerProAsnValCysHisSerAsnIleTyrSer 260
 DB 1048 GAGTACAGCGCGCGACTTGTGAGGTGTCCCAATGTGTGCCACAGCAATATCTATTTCA 1107
 QY 261 ProLysGluThrIleProGluGluValArgSerAspMetHisTyrSerValIleGluGly 280
 DB 1108 CCCAAGGAAACATCCCAAGAGAGCGACAGATGATGTGCACTACGTGTGGCTGAGGCGC 1167
 QY 281 LeuLysProAlaAlaProSerAlaArgAsnAlaProTyrPheProCysAspLysAlaSer 300
 DB 1168 CTCAAACTGTGCGCCCTCAAGCCCAATGCCCCCTCACTTCCCTGTGACAGAGCCAGC 1227
 QY 301 LysGluGluGluArgProSerSerGluAspGluIleAlaLeuHisPheGluProProAsn 320
 DB 1228 AAAGAAAGAGAGACCTCTCTCGAAGATGAGATTCTCTGCAATTTGAGAGCCCCCAAT 1287
 QY 321 AlaProLeuAsnArgLysGlyLeuValSerProGlnSerProGlnLysSerAspCysGln 340
 DB 1288 GCACCTCTGAACGGAAGGCTGTGTATGTCACAGAGCCCCCAGAAATCTGATGCGAG 1347

QY 341 ProAsnSerProThrGluAlaCysSerSerLysAsnAlaCysIleLeuGlnAlaSerGly 360
 DB 1348 CCCAATCGGCCACAGAGCGCTGACAGAGTGAAGATGCTGTATCTTCAAGCTTCTGCG 1407
 QY 361 SerProProAlaLysSerProThrAspProLysAlaCysAsnTyrLysIleTyrLysPhe 380
 DB 1408 TCCCTCCAGCCAAAGAGCCCACTGACCCCAAGCTGTCACTGAGAAATATCAAGTTTC 1467
 QY 381 IleValLeuAsnSerLeuAsnGlnAsnAlaLysProGlyGlyProGluGlnAlaGluLeu 400
 DB 1468 ATCGTGCTCAAGAGCTCAACAGATGCAAAACAGGGGGGCGTAGAGAGCTGAGCTG 1527
 QY 401 GlyArgLeuSerProArgAlaTyrThrAlaProProAlaCysGlnProMetGluPro 420
 DB 1528 GCGCCCTTTCCTCCAGAGCTTACAGCGCCCACTGCTGCTGACCAACCCATGAGGCT 1587
 QY 421 GluAsnLeuAspLeuGlnSerProThrLysLeuSerAlaSerGlyGluAspSerThrIle 440
 DB 1588 GAAACCTTGACCTCAAGTCCCAACAGCTGAGTGCAGCGGAGAGAGACTTCACATC 1647
 QY 441 ProGlnAlaSerArgLeuAsnAsnIleValAsnArgSerMetThrGlySerProArgSer 460
 DB 1648 CCACAGCCAGCGGCTCAATACATCGTTAACAGTCCATGACGAGGCTCTCCCGCAGC 1707
 QY 461 SerSerGluSerHisSerProLeuTyrMetHisProProLysCysThrSerCysGlySer 480
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 QY 481 GlnSerProGlnHisAlaGluMetCysLeuHisThrAlaGlyProThrPheAlaGluGly 500
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 DB 1828 ATGGAGAGAGCCCACTGAGTCAATCAATTTACTGCTGAGAACGGGCTTCTTCTGCG 1887
 QY 521 AsnGluCysAspCysArgPheSerGluGluAlaSerLeuLysValArgHisThrLeuGlnThr 540
 DB 1888 AATGATGTGATGCTGCGCTTCTCTGAGAGGCTCTCACTCAAGAGCACAGCTGCAGACC 1947
 QY 541 HisSerAspLysProTyrLysCysAspArgCysGlnAlaSerPheArgTyrLysGluAsn 560
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 DB 2008 CTGCGCAGCACAAGACCTTCATACCGGTGAGAAACCTTACGTTGCAACATCTGTGG 2067
 QY 581 AlaGlnPheAsnArgProAlaAsnLeuLysThrHisThrArgIleHisSerGlyGluLys 600
 DB 2068 GCCCAATTCACACGCGCAGCCCACTGAAACCCACACTGAAATCACTCTGAGAGAGAG 2127
 QY 601 ProTyrLysCysGluThrCysGlyValaArgPheValGlnValAlaHisLeuArgAlaHis 620
 DB 2128 CCTTAAATATGGAACCTGCGAGCGCAATTTGTACAGGTGACCCACCTCTGCTGCCAT 2187
 QY 621 ValLeuIleHisThrGlyGluLysProTyrProCysGluIleCysGlyThrArgPheArg 640
 DB 2188 GTGCTTATCAACATGTGTGAGAGGCTTATCTCTGTGAATGTGTGTGAGCACCGGTTCCG 2247
 QY 641 HisLeuGlnThrLeuLysSerHisLeuArgIleHisThrGlyGluLysProTyrHisCys 660
 DB 2248 CACCTTCAAGCTTGAAGAGCACTGCAATTCACACAGAGAGAGAAACCTTACCACTTGT 2307
 QY 661 GluLysCysAsnLeuHisPheArgHisIleLysSerGlnLeuArgLeuHisLeuArgGluLys 680
 DB 2308 GAGAAAGTGAACCTGTGATTTCCGTCAAAAGCGCACTGCACTTCACTTGGCCAGAG 2367
 QY 681 HisGlyAlaIleThrAsnThrLysValGlnTyrArgValSerAlaThrAspLeuProPro 700
 DB 2368 CATGGCGCATACACAGACCAAGGTGCAATCCGGGTGTGAGCCACTGACCTGCTCGG 2427

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus.p2n model

Run on: March 2, 2006, 02:10:16 ; Search time 582 Seconds
(without alignments)
2659.480 Million cell updates/sec

Title: US-10-755-889-18
Perfect score: 3793
Sequence: 1 MASPADSCQFTTHASDVLL.....TKYQYVSAVDLPPELPKAC 706

Scoring table:
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7218512 seqs, 109618070 residues
Total number of hits satisfying chosen parameters: 14437024

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/abes/ASSWEB.spool/US10755889/rnat.01032006.143957.11563/app_query.fasta.1
-DB=Published Applications NA New -QFMT=fastap -SUFFIX=p2n.rmpbn -MINMATCH=0.1
-LOOPC=0 -LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62
-TRANS=human40.cdi -LIST=45 -LOCAL=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abes06p
-USER=US10755889 @CGN 1 1 335 @rnat.01032006.143957.11563 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA New:*

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12: /cgn2_6/ptodata/1/pubpna/US11 NEW PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US60 NEW PUB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
1	3793	100.0	3536	12	US-11-122-329-70 Sequence 70, Appl
2	503	13.3	3052	9	US-11-072-512-959 Sequence 959, Appl
3	475	12.5	2435	12	US-11-000-688-1136 Sequence 1136, Ap
4	474.5	12.5	2784	9	US-11-072-512-1944 Sequence 1944, Ap

5	473	12.5	3090	9	US-11-072-512-191	Sequence 191, Appl
6	472.5	12.5	1578	12	US-11-136-527-2436	Sequence 2436, Ap
7	468.5	12.4	2110	9	US-11-072-512-1778	Sequence 1778, Ap
8	465.5	12.3	3026	9	US-11-072-512-967	Sequence 967, Appl
9	465	12.3	3078	9	US-11-072-512-622	Sequence 622, Appl
10	464	12.2	2724	9	US-11-072-512-1127	Sequence 1127, Ap
11	464	12.2	2744	7	US-10-517-151-3	Sequence 3, Appl
12	463.5	12.2	2241	9	US-11-072-512-693	Sequence 693, Appl
13	462.5	12.2	2467	9	US-11-072-512-470	Sequence 470, Appl
14	462.5	12.2	2634	9	US-11-072-512-816	Sequence 816, Appl
15	462	12.2	4305	8	US-10-750-185-44166	Sequence 44166, A
16	462	12.2	4305	8	US-10-750-623-44166	Sequence 44166, A
17	461.5	12.2	1833	9	US-11-072-512-1491	Sequence 1491, Ap
18	460.5	12.1	3335	9	US-11-072-512-522	Sequence 522, Appl
19	459.5	12.1	2918	9	US-11-072-512-835	Sequence 835, Appl
20	458	12.1	1914	9	US-11-072-512-1464	Sequence 1464, Ap
21	457.5	12.1	2603	12	US-11-000-688-1179	Sequence 1179, Ap
22	457.5	12.1	193789	12	US-11-112-908-55	Sequence 55, Appl
23	457	12.0	1694	9	US-11-072-512-1500	Sequence 1500, Ap
24	456.5	12.0	648	6	US-09-925-065A-418152	Sequence 418152, A
25	454.5	12.0	2509	6	US-09-925-065A-87059	Sequence 87059, A
26	454.5	12.0	2537	9	US-11-072-512-1179	Sequence 1179, Ap
27	454.5	12.0	3138	9	US-11-072-512-83	Sequence 83, Appl
28	454	12.0	3301	9	US-11-072-512-479	Sequence 479, Appl
29	453.5	12.0	648	6	US-09-925-065A-418150	Sequence 418150, A
30	450.5	11.9	648	6	US-09-925-065A-418151	Sequence 418151, A
31	450.5	11.9	2042	9	US-11-072-512-1396	Sequence 1396, Ap
32	450.5	11.9	3400	9	US-11-072-512-1037	Sequence 1037, Ap
33	450	11.9	3492	6	US-09-925-065A-47571	Sequence 47571, A
34	450	11.9	3492	6	US-09-925-065A-47572	Sequence 47572, A
35	449.5	11.9	2252	8	US-10-750-185-58156	Sequence 58156, A
36	449.5	11.9	2252	8	US-10-750-623-58156	Sequence 58156, A
37	448	11.8	600	12	US-11-136-527-6532	Sequence 6532, Ap
38	448	11.8	2985	12	US-11-122-329-116	Sequence 116, Appl
39	447.5	11.8	2357	9	US-11-072-512-1701	Sequence 1701, Ap
40	446.5	11.8	2668	12	US-11-136-527-2016	Sequence 2016, Ap
41	445	11.7	2698	9	US-11-072-512-271	Sequence 271, Appl
42	445	11.7	2857	12	US-11-136-527-360	Sequence 360, Appl
43	443.5	11.7	2509	6	US-09-925-065A-87058	Sequence 87058, A
44	442.5	11.7	732	6	US-09-925-065A-918557	Sequence 918557, A
45	442.5	11.7	732	6	US-09-925-065A-918560	Sequence 918560, A

ALIGNMENTS

RESULT 1
US-11-122-329-70
Sequence 70, Application US/11122329
Publication No. US20060019272A1
GENERAL INFORMATION:
APPLICANT: Geraci, Mark
APPLICANT: Bull, Todd
APPLICANT: Voelkel, Norbert
TITLE OF INVENTION: Diagnosis of Disease and Monitoring of Therapy Using Gene
FILE REFERENCE: 2448-54
CURRENT APPLICATION NUMBER: US/11/122,329
PRIOR FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/568,129
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PatentIn version 3.3
SEQ ID NO 70
LENGTH: 3536
TYPE: DNA
ORGANISM: Homo sapiens
US-11-122-329-70
Alignment Scores:
Pred. No.: 6.47e-240 Length: 3536
Score: 3793.00 Matches: 706
Percent Similarity: 100.0% Conservative: 0

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 2, 2006, 03:45:47 ; Search time 187 Seconds
(without alignments)
1658.831 Million cell updates/sec

Title: US-10-755-889-18

Perfect score: 3793
Sequence: 1 MASPDSCIQFTTHASDVLL.....TKVQVRVSATDLPPELPKAC 706

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: A_Geneseq_21.*
- 2: geneseqp1980a.*
- 3: geneseqp1990a.*
- 4: geneseqp2000a.*
- 5: geneseqp2001a.*
- 6: geneseqp2002a.*
- 7: geneseqp2003a.*
- 8: geneseqp2004a.*
- 9: geneseqp2005a.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	3793	100.0	706	8	ADL82847 Human PRO
4	3793	100.0	706	8	ADL82847 Human PRO
5	3793	100.0	706	8	ADL82847 Human PRO
6	3777	99.6	706	9	ADY15990 PRO polyp
7	3777	99.6	706	9	ADY15990 PRO polyp
8	3771	99.4	706	7	ADY15006 PRO polyp
9	3763	99.2	706	2	AAE68743 BCL-6 zin
10	3763	99.2	706	3	AAV78792 Human BCL
11	3602.5	95.0	707	5	AB57289 Mouse lbc
12	1158.5	30.5	458	8	ABM84710 Human dla
13	1155	30.5	479	6	ABU03467 Angiogene
14	1155	30.5	479	6	ABU03467 Angiogene
15	1155	30.5	479	6	ABU03467 Angiogene
16	1155	30.5	479	6	ABU03467 Angiogene
17	1151.5	29.9	480	7	AAO16438 Human nuc
18	1135.5	29.9	480	7	ABU64322 AAC2-1 pr
19	1135.5	29.9	480	8	ADU99228 AAC2-1 tu
20	1132.5	29.6	518	4	AAE11887 Angiogene
21	912.5	24.1	362	9	AAE20968 Novel hum
22	678.5	17.3	667	8	ADP22538 Sea-squir
23	658	17.3	129	9	ABE10947 Human BCL
24	658	17.3	129	9	ABE10971 Human BTB

25	618.5	16.3	810	3	AAV73351	AAV73351 HTRM clon
26	610	16.1	803	7	ADD45510	Add45510 Human pro
27	610	16.1	803	8	ADG30638	Adg30638 Human tub
28	609	16.1	803	4	AAH39272	Aah39272 Human pol
29	609	16.1	804	4	AAH41058	Aah41058 Human pol
30	602	15.9	803	2	AAH810948	Aah810948 Human BCL
31	602	15.9	803	2	AAH810948	Aah810948 Human BCL
32	588	15.5	756	7	ADP17459	Adp17459 Myc-blnd1
33	564.5	14.9	765	6	ABP96329	Abp96329 Human nuc
34	560	14.8	765	8	ADP09346	Adp09346 Human pro
35	540	14.2	688	5	ABH82513	Abh82513 Human rep
36	535	13.8	775	7	ADC31774	Adc31774 Human nov
37	522.5	13.8	603	4	AAH41821	Aah41821 Human pro
38	522.5	13.8	610	4	AAH53761	Aah53761 Human pro
39	522.5	13.8	610	4	ABH50159	Abh50159 Human tra
40	522.5	13.8	610	5	AAH47779	Aah47779 Human myo
41	522.5	13.8	610	5	AAH47790	Aah47790 Murine my
42	522.5	13.8	610	5	AAH47790	Aah47790 Murine my
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44	517	13.6	711	5	AAO21779	Aao21779 Lung-spec
45	517	13.6	711	9	ADY71945	Ady71945 Human GZF

ALIGNMENTS

RESULT 1

AAV78793 standard; protein; 706 AA..

AAV78793;

19-MAY-2000 (first entry)

Human BCL-6 protein sequence.

Bcl-6; human; B-cell lymphoma; regulator; non-Hodgkin's lymphoma;

diffuse type B-cell lymphoma.

Homo sapiens.

MO200000185-A1.

06-JUN-2000.

30-JUN-1999; 99MO-US014703.

30-JUN-1998; 98US-00107058.

(UYCO) UNIV COLUMBIA NEW YORK.

Dalla-Favera R, Niu H;

WPI; 2000-160631/14.

Novel methods for regulating BCL-6 levels in cells used to treat humans with lymphoma.

Example 2; Fig 10; 159pp; English.

This sequence represents the human bcl-6 protein sequence. The invention relates to a vertebrate bcl-6 locus which is the breakpoint cluster region in B-cell lymphomas, and contains a bcl-6 gene encoding a BCL-6 polypeptide. Administration of a molecule which induces phosphorylation of BCL-6 and thereby induces BCL-6 degradation, can be used as a method of regulating BCL-6 in cells. The methods of the invention can be used to regulate, and especially to decrease BCL-6 levels in cells. The methods may also be used to screen putative therapeutic agents for treatment of non-Hodgkin's lymphoma, by contacting cells from lymphoma and normal cells with the agent, and after a period of time comparing the amount of bcl-6 nucleic acid in each sample, a difference indicating the effectiveness of the agent. The bcl-6 gene is a source of probes and B primers, which are used to diagnose diffuse-type B cell lymphoma and B

Attachment 1

XX	Homo sapiens.
OS	
XX	
PN	US6140125-A.

PD	31-OCT-2000.
XX	
PF	15-OCT-1999;

99US-00418640.

PR 15-OCT-1999;
XX
PA (ISIS-) ISIS

99US-00418640.
PHARM INC.

PI	Taylor JK, C
XX	
DR	WPI; 2001-048
DR	WPI; 2001-048

Lowbert LM;
3959/06.

XX	Antisense con
PT	bcl-6 express
PT	overexpres

compounds which specifically hybridize with and inhibit human bcl-6 expression, useful for treating bcl-6 related disorders, and delaying inflammation or tumor formation.

XX
PS Disclosure; C
XX
CC This sentence

vol 47-52; 42pp; English.
representative human vol-6 Bc]-6 (a) so known as B-co]]

CC	CLL/Lymphoma
CC	DNA-binding to
CC	germinal center
CC	formation and

Th-2 mediated antibody affinity maturation. Bcl-6 may also mediate B- and T-cell and is required for germinal centre transcriptional repressor. The bcl-6 gene is expressed in

CC play a role in
CC chromosome 3q
CC translocation
CC aberrant form

of bcl-6, which are strongly implicated in the regulation of apoptosis. The bcl-6 gene is located on chromosome 2p25, a region which undergoes a high frequency of chromosomal translocations can result in events. Such chromosomal translocations can result in

CC parvoviruses
CC acute lymphob
CC disorders. Th
CC to the human

of several types of lymphoma, and have also been reported in myeloid leukaemia and post-transplant lymphoproliferative disease. The *bcl-6* gene, which inhibits its expression. A series of

regions of the
bcl-6 mRNA le
the invention

are useful for diagnosis, prevention and treatment of

acute lymphoblastic disorders

Elastic leukaemia and post-transplant lymphoproliferative

Query Match
Best Local Simil

100.0%; Score 3793; DB 4; Length 706;
100.0%; Pred. No. 9.8e-284;

QY 1 MASF
|||||

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	61	FTDQ
QY		
DH		

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QY	121	CRKF
dh	121	CPKF

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KASEAEMVSAIKPPREEFLNSRMLMPQODIMAYRGREVENNLPLRSAPGESRAF 1800
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QY	181	APSL
Db	181	APSL

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YSGSLSTBPASYSMTSHLPVSSLLFSDSEFRDVRMPVANPFPKERALPCDSARPVG 240

QY	241	EYSR
DB	241	EYSR

PTLEVSPNVCHSNTYSPKETIPBEARSDMHYVAEGLKPAAPSAARNAPYPPCDKAS 300

QY 301 XEEE
||||

RPSSSEDEIALHFEDPNALPNRKGLVSPQSPQSDCQPNSPTEACSKNACILQASG 360

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